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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query length: 289 AA

Date run: 2004-03-23 06:06:22 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProt

1,414,857 sequences; 451,237,162 total letters

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List of potentially matching sequences

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Db AC	Description	Score	E-value
<input type="checkbox"/> sp P43716	ATPG_HAEIN ATP synthase gamma chain (EC 3.6.3.14) [ATP...	562	e-159
<input type="checkbox"/> sp Q9L6B6	ATPG_PASMU ATP synthase gamma chain (EC 3.6.3.14) [ATP...	456	e-127
<input type="checkbox"/> tr Q7VPP1	ATP synthase gamma chain [ATPG] [Haemophilus ducreyi]	438	e-122
<input type="checkbox"/> sp P00837	ATPG_ECOLI ATP synthase gamma chain (EC 3.6.3.14) [ATP...	390	e-107
<input type="checkbox"/> tr Q8ZKW8	Membrane-bound ATP synthase, F1 sector, gamma-subunit ...	389	e-107
<input type="checkbox"/> tr Q9RFL4	ATP synthase subunit gamma [ATPG] [Salmonella typhimur...	389	e-107
<input type="checkbox"/> tr Q7NA93	ATP synthase gamma chain [ATPG] [Photorhabdus luminesc...	387	e-106
<input type="checkbox"/> tr Q8E8B9	ATP synthase F1, gamma subunit [ATPG] [Shewanella onei...	385	e-106
<input type="checkbox"/> tr Q8Z2Q5	ATP synthase gamma subunit [STY3912] [Salmonella typhi]	385	e-106
<input type="checkbox"/> tr Q8Z9S5	ATP synthase gamma subunit protein (EC 3.6.1.34) (Memb...	381	e-105

<input type="checkbox"/>	tr Q9KNH4	ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae]	376	e-103
<input type="checkbox"/>	tr Q7MGH9	F0F1-type ATP synthase, gamma subunit [VV3252] [Vibrio...	375	e-103
<input type="checkbox"/>	tr Q8DDG9	ATP synthase F1, gamma subunit [VV11020] [Vibrio vulni...	375	e-103
<input type="checkbox"/>	tr Q87KA7	ATP synthase F1, gamma subunit [VP3070] [Vibrio paraha...	374	e-102
<input type="checkbox"/>	sp P12990	ATPG_VIBAL ATP synthase gamma chain (EC 3.6.3.14) [ATP...	373	e-102
<input type="checkbox"/>	tr Q9HT19	ATP synthase gamma chain [ATPG] [Pseudomonas aeruginosa]	362	5e-99
<input type="checkbox"/>	tr Q8VV78	F0F1-ATPase subunit gamma [ATPG] [Colwellia maris (Vib...	353	2e-96
<input type="checkbox"/>	tr Q88BX3	ATP synthase F1, gamma subunit [ATPG] [Pseudomonas put...	349	2e-95
<input type="checkbox"/>	tr Q87TT3	ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syr...	347	9e-95
<input type="checkbox"/>	tr Q83AF6	ATP synthase, F1 gamma subunit [ATPG] [Coxiella burnetii]	338	4e-92
<input type="checkbox"/>	tr Q82XP9	ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Nitro...	337	1e-91
<input type="checkbox"/>	tr Q8XU75	Probable ATP synthase gamma chain protein (EC 3.6.1.34...	331	9e-90
<input type="checkbox"/>	tr Q8PCZ6	ATP synthase gamma chain [ATPG] [Xanthomonas campestri...	323	2e-87
<input type="checkbox"/>	sp Q51873	ATPG_BUCAP ATP synthase gamma chain (EC 3.6.3.14) [ATP...	322	3e-87
<input type="checkbox"/>	sp P57123	ATPG_BUCAI ATP synthase gamma chain (EC 3.6.3.14) [ATP...	322	3e-87
<input type="checkbox"/>	tr Q8PGG6	ATP synthase gamma chain [ATPG] [Xanthomonas axonopodi...	318	5e-86
<input type="checkbox"/>	tr Q87E89	ATP synthase gamma chain [ATPG] [Xylella fastidiosa (s...	305	5e-82
<input type="checkbox"/>	tr Q9PE84	ATP synthase, gamma chain [XF1144] [Xylella fastidiosa]	305	5e-82
<input type="checkbox"/>	tr Q7VU45	ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete...	304	9e-82
<input type="checkbox"/>	tr Q7WEM8	ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete...	304	1e-81
<input type="checkbox"/>	tr Q7W3A9	ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordete...	303	2e-81
<input type="checkbox"/>	tr Q7VQV7	ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Candi...	302	3e-81
<input type="checkbox"/>	sp P41169	ATPG_THIFE ATP synthase gamma chain (EC 3.6.3.14) [ATP...	301	8e-81
<input type="checkbox"/>	tr Q7P096	H ⁺ -transporting two-sector ATPase, gamma subunit (EC 3...	300	2e-80
<input type="checkbox"/>	tr Q83U82	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	297	1e-79
<input type="checkbox"/>	tr Q83V88	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	296	2e-79
<input type="checkbox"/>	tr Q83V83	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	296	2e-79
<input type="checkbox"/>	tr Q83V86	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	295	4e-79
<input type="checkbox"/>	tr Q9RQ80	Gamma subunit of membrane-bound ATP synthase [ATPG] [B...	295	4e-79
<input type="checkbox"/>	tr Q9JW71	ATP synthase gamma chain (EC 3.6.1.34) [ATPG] [Neisser...	295	5e-79
<input type="checkbox"/>	tr Q83U83	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	295	5e-79
<input type="checkbox"/>	tr Q9JXQ1	ATP synthase F1, gamma subunit [NMB1935] [Neisseria me...	295	7e-79
<input type="checkbox"/>	tr Q83V85	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	294	9e-79
<input type="checkbox"/>	tr Q83V87	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	294	1e-78
<input type="checkbox"/>	tr Q83UA6	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	293	2e-78
<input type="checkbox"/>	tr Q83V84	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	293	2e-78
<input type="checkbox"/>	tr Q83V89	ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Hae...	292	4e-78
<input type="checkbox"/>	tr Q9RQ74	Gamma subunit of membrane-bound ATP synthase [ATPG] [B...	268	9e-71
<input type="checkbox"/>	tr Q8D3J4	AtpG protein [ATPG] [Wigglesworthia glossinidia brevip...	265	8e-70
<input type="checkbox"/>	sp Q89B40	ATPG_BUCBP ATP synthase gamma chain (EC 3.6.3.14) [ATP...	261	9e-69
<input type="checkbox"/>	tr Q9RQ77	Gamma subunit of membrane-bound ATP synthase [ATPG] [B...	256	3e-67
<input type="checkbox"/>	tr Q831A4	ATP synthase F1, gamma subunit [ATPG] [Enterococcus fa...	218	8e-56
<input type="checkbox"/>	sp P20602	ATPG_BACME ATP synthase gamma chain (EC 3.6.3.14) [ATP...	216	4e-55
<input type="checkbox"/>	tn AAQ10089	ATP synthase subunit gamma [ATPG] [Bacillus sp. TA2.A1]	211	1e-53
<input type="checkbox"/>	tr Q8E5U9	H ⁺ -transporting ATP synthase gamma chain [ATPG] [Strep...	210	2e-53

<input type="checkbox"/>	sp	Q9K6H4	ATPG_BACHD ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	209	4e-53
<input type="checkbox"/>	tr	Q8E073	ATP synthase F1, gamma subunit [ATPG] [Streptococcus a...	208	9e-53
<input type="checkbox"/>	tr	Q814W1	ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bacil...	207	1e-52
<input type="checkbox"/>	tr	Q81JZ4	ATP synthase F1, gamma subunit [ATPG] [Bacillus anthra...	207	1e-52
<input type="checkbox"/>	tn	AAS44331	ATP synthase F1, gamma subunit (EC 3.6.3.14) [ATPG] ...	207	1e-52
<input type="checkbox"/>	tr	Q9RAU1	H+-ATPase cytoplasmic F1-part gamma-subunit (H+-ATPase...	206	3e-52
<input type="checkbox"/>	tr	Q8EM82	H(+)-transporting ATP synthase gamma chain (EC 3.6.1.3...	206	4e-52
<input type="checkbox"/>	sp	Q9CER9	ATPG_LACLA ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	205	7e-52
<input type="checkbox"/>	sp	P22482	ATPG_BACPF ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	205	7e-52
<input type="checkbox"/>	tr	Q8CNJ6	ATP synthase gamma chain [SE1701] [Staphylococcus epid...	205	7e-52
<input type="checkbox"/>	tr	O05432	ATP synthase subunit gamma [ATPG] [Moorella thermoacet...	204	1e-51
<input type="checkbox"/>	sp	P09222	ATPG_BACP3 ATP synthase gamma chain precursor (EC 3.6....	202	6e-51
<input type="checkbox"/>	tr	Q9A0I8	Putative proton-translocating ATPase, gamma subunit (E...	201	8e-51
<input type="checkbox"/>	tr	Q52412	TF1-gamma subunit [thermophilic bacterium PS3]	201	1e-50
<input type="checkbox"/>	sp	P37810	ATPG_BACSU ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	201	1e-50
<input type="checkbox"/>	tr	Q99SF4	ATP synthase gamma chain [ATPG] [Staphylococcus aureus...	201	1e-50
<input type="checkbox"/>	tr	O50158	Proton-translocating ATPase, gamma subunit [ATPG] [Str...	201	1e-50
<input type="checkbox"/>	tr	Q8K827	Putative proton-translocating ATPase gamma subunit [SP...	200	2e-50
<input type="checkbox"/>	tr	Q84XB4	Chloroplast ATPase gamma subunit precursor [ATPC] [Pha...	200	2e-50
<input type="checkbox"/>	sp	P12408	ATPG_ANASP ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	198	9e-50
<input type="checkbox"/>	sp	P41010	ATPG_BACCA ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	197	2e-49
<input type="checkbox"/>	sp	P42007	ATPG_BACST ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	196	3e-49
<input type="checkbox"/>	tr	Q927W3	AtpG protein [ATPG] [Listeria monocytogenes, Listeria ...	195	6e-49
<input type="checkbox"/>	sp	P29710	ATPG_PROMO ATP synthase gamma chain, sodium ion specif...	194	2e-48
<input type="checkbox"/>	sp	Q41075	ATPG_PHATR ATP synthase gamma chain, chloroplast precu...	194	2e-48
<input type="checkbox"/>	sp	Q06908	ATPG_ODOSI ATP synthase gamma chain, chloroplast precu...	194	2e-48
<input type="checkbox"/>	tr	Q8FQ21	H+-ATPase gamma subunit (EC 3.6.3.14) [ATPG] [Coryneba...	194	2e-48
<input type="checkbox"/>	tr	Q8KRU9	Subunit gamma [ATPG] [Ilyobacter tartaricus]	194	2e-48
<input type="checkbox"/>	sp	P43452	ATPG_ENTHR ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	193	3e-48
<input type="checkbox"/>	tr	Q8KAW9	ATP synthase F1, gamma subunit [ATPG] [Chlorobium tepi...	192	5e-48
<input type="checkbox"/>	tr	Q8RKV3	H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG] [St...	192	5e-48
<input type="checkbox"/>	sp	P08450	ATPG_SYNP6 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	191	8e-48
<input type="checkbox"/>	sp	Q05384	ATPG_SYNP1 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	191	1e-47
<input type="checkbox"/>	tr	Q8DLU1	H+-transporting ATP synthase gamma chain [ATPC] [Synec...	191	1e-47
<input type="checkbox"/>	sp	P17253	ATPG_SYNY3 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] ...	190	2e-47
<input type="checkbox"/>	tr	Q7NDC0	ATP synthase gamma chain [ATPC] [Gloeobacter violaceus]	190	2e-47
<input type="checkbox"/>	sp	P50005	ATPG_ACEWO ATP synthase gamma chain, sodium ion specif...	189	4e-47
<input type="checkbox"/>	tr	Q7P5L4	ATP synthase gamma chain, sodium ion specific (EC 3.6....	189	4e-47
<input type="checkbox"/>	tr	Q97PT5	ATP synthase F1, gamma subunit (Proton-translocating A...	189	5e-47
<input type="checkbox"/>	tr	Q8RGE1	ATP synthase gamma chain, sodium ion specific (EC 3.6....	187	1e-46
<input type="checkbox"/>	tr	Q7MA19	ATP synthase F1 gamma subunit (EC 3.6.3.14) [ATPG] [Wo...	187	2e-46
<input type="checkbox"/>	tr	Q9ZJ02	Proton-translocating ATPase gamma subunit [Streptococc...	186	3e-46
<input type="checkbox"/>	tr	Q9FDR6	H+-ATPase gamma subunit (F0F1-type ATP synthase gamma ...	186	4e-46
<input type="checkbox"/>	tr	Q9FAA4	H+-ATPase gamma subunit [ATPG] [Brevibacterium flavum]	186	4e-46
<input type="checkbox"/>	tn	CAF19915	ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.3.14) [ATPG] [Cor...	186	4e-46

Graphical overview of the alignments

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or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

ATP-synt

Submission	Matches on query sequence										Mat
	1	50	100	150	200	250					1
ATPG_HREIN											
ATPG_PASMU											
Q7VPP1											
ATPG_ECOLI											
Q8ZKM8											
Q9RFL4											
Q7NA93											
Q8E889											
Q8Z2Q5											
Q8Z9S5											
Q9KNH4											
Q7MGR9											
Q8DDG9											
Q87KA7											
ATPG_VIBAL											
Q9HT19											
Q8VV78											
Q88BX3											
Q87TT3											
Q83AF6											
Q82XP9											
Q8XU75											
Q8PCZ6											
ATPG_BUCAP											
ATPG_BUCAI											
Q8PGG6											
Q87E89											
Q9PE84											
Q7VU45											
Q7MEM8											
Q7H3A9											
Q7VQV7											
ATPG_THIFE											
Q7P096											
Q83U82											
Q83V88											
Q83V83											
Q83V86											
Q9RQ80											
Q9JW71											
Q83U83											
Q9JXQ1											
Q83V85											
Q83V87											
Q83U86											
Q83V84											
Q83V89											
Q9RQ74											
Q8D3J4											
ATPG_BUCBP											
Q9RQ77											
Q831A4											
ATPG_BACHE											
AAQ10089											
Q8E5U9											
ATPG_BACHD											
Q8E073											
Q814M1											
Q81JZ4											
AA544331											
Q9RAU1											
Q8EM82											
ATPG_LACLA											
ATPG_BACPF											
Q8CNJ6											
Q05432											
ATPG_BACP3											
Q9A0I8											
Q52412											
ATPG_BACSU											
Q99SF4											
Q50158											
Q8K827											
Q84XB4											
ATPG_ANASP											
ATPG_BACCA											
ATPG_BACST											
Q927H3											
ATPG_PROMO											
ATPG_PHATR											
ATPG_ODOSI											
Q8FQ21											
Q8KRU9											
ATPG_ENTHR											
Q8KAH9											
Q8RKV3											

Alignments

sp P43716 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Haemophilus 289 AA
ATPG_HAEIN influenzae]

[align](#)

Score = 562 bits (1448), Expect = e-159
Identities = 289/289 (100%), Positives = 289/289 (100%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS
Sbjct: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS
Sbjct: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS
Sbjct: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS
Sbjct: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI
Sbjct: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

sp Q9L6B6 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Pasteurella 289 AA
ATPG_PASMU multocida]

[align](#)

Score = 456 bits (1173), Expect = e-127
Identities = 221/289 (76%), Positives = 263/289 (90%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI+TKIASV+STQKITKAMEMVA SKMRKTQ+RM++SRPYSETIRNVISHVSKA+
Sbjct: 1 MAGAKEIRTKIASVKSTQKITKAMEMVAASKMRKTQERMSSSRPYSETIRNVISHVSKAT 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
IGYKHPFLV+REVKK+G++V+STDRG+CGGLNVNLFKT LN++K WKE+++S L LIGS
Sbjct: 61 IGYKHPFLVDREVKKVGMIVVSTDRGLCGGLNVNLFKTVLNEMKEWKEKDVSQVLSLIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K I+FF+S G I Q SG+GDTP++E+LIG N+M DAY+ GE+D VY+ YNKF+NTMS
Sbjct: 121 KSINFFQSLGIKILTQDSGIGDTPSVEQLIGSVNSMIDAYKKGEVDVVYLVYNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
QKPV+++L+PLPE +D L ER+Q WDY+YEP+ KVLLD+LLVRYLESQ+YQA V+N+AS
Sbjct: 181 QKPVLEKLIPLPELDNDELGERKQVWDYIYEPDAKVLLDNLLVRYLESQVYQAAVENLAS 240

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNAGNLIN+L+LVYNKARQASITNELNEIVAGAAAI

Sbjct: 241 EQAARMVAMKAATDNAGNLINELQLVYNKARQASITNELNEIVAGAAAI 289

tr Q7VPP1 ATP synthase gamma chain [ATPG] [Haemophilus 288 AA
ducreyil] align

Score = 438 bits (1127), Expect = e-122

Identities = 212/289 (73%), Positives = 259/289 (89%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI+TKIASV++TQKITKAMEMVATSKMRKTQ+RMAA RPYSETIR VISH++K S
Sbjct: 1 MAGAKEIRTKIASVRNTQKITKAMEMVATSKMRKTQERMAAGRPYSETIRKVISHIAKGS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
IGYKHPFL+ER+VKK+G LVISTDRG+CGGLN+NLFKTTLN+ K WK++++S +LGL+GS
Sbjct: 61 IGYKHPFLIERDVKKVGYLVISTDRGLCGGLNINLFKTTLNEFKAWKDKDVSVELGLVGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG+SF++S G ++ ++GLGD+P +E ++G N M +AYRNGE+D V IAYN+F NTMS
Sbjct: 121 KGVSFYQSIGLKVRAHITGLGDSPEMERIVGAVNEMINAYRNGEVDMVCIAYNRFENTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
QK V+ QL+PLP+ ++D L E + +WDYLYEP P+VLLDSSL+RYLE+Q+YQAVVDN+AS
Sbjct: 181 QKTVIAQLLPLPKLENDEL-ETKCSWDYLYEPNPQVLLDSSLIRYLETQVYQAVVDNLAS 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNAG LI++L+LVYNKARQASITNELNEIVAGAAAI
Sbjct: 240 EQAARMVAMKAATDNAGALIDELQLVYNKARQASITNELNEIVAGAAAI 288

sp P00837 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Escherichia 287
ATPG_ECOLI coli, AA
Escherichia coli O6, Escherichia coli O157:H7, Shigella align
flexneri]

Score = 390 bits (1001), Expect = e-107

Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +
Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ YKHP+L +R+VK++G LV+STDRG+CGGLN+NLFK L ++K W ++ + DL +IGS
Sbjct: 61 LEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFKLLAEMKTWTDKGVQCDLAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
Sbjct: 121 KGVSFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRDLKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
Q P + QL+PLP S DD L + ++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS
Sbjct: 181 QVPTISQLLPLPASDDDDL--KHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

tr Q8ZKW8 **Membrane-bound ATP synthase, F1 sector, gamma-subunit (EC 287**
3.6.3.14) **AA**
[ATPG] [Salmonella typhimurium] align

Score = 389 bits (999), Expect = e-107

Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +
Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLANGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ YKHP+L ER+VK++G LV+STDRG+CGGLN+NLFK L +K W ++ + +L +IGS
Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDRGLCGGLNINLFFKLLADMKAWSDKGVQCELAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
Sbjct: 121 KGVSFNFSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRDLKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
Q P + QL+PLP S+DD L +++ WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS
Sbjct: 181 QVPTITQLLPLPASEDDDL--KRKAWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

tr Q9RFL4 **ATP synthase subunit gamma [ATPG] [Salmonella typhimurium] 287 AA**
align

Score = 389 bits (999), Expect = e-107

Identities = 188/289 (65%), Positives = 237/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +
Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ YKHP+L +R+VK++G LV+STDRG+CGGLN+NLFK L ++K W ++ + DL +IGS
Sbjct: 61 LEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFFKLLAEMKTWTDKGVQCDLAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
Sbjct: 121 KGVSFNFSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRDLKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
Q P + QL+PLP S DD L + ++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS
Sbjct: 181 QVPTISQLLPLPASDDDDL--KHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
 Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

tr Q7NA93 **ATP synthase gamma chain [ATPG] [Photorhabdus luminescens** 287
 (subsp. AA
 laumondii)] align

Score = 387 bits (994), Expect = e-106
 Identities = 188/289 (65%), Positives = 238/289 (82%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEI+TKIASVQ+TQKITKAMEMVA SKMRKTQDRMAASRPY+ETIR+VI H++ +
 Sbjct: 1 MAGAKEIRTKIASVQNTQKITKAMEMVAASKMRKTQDRMAASRPYAETIRSVIGHLALGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKHP+L ERE K++G LV+STDRG+CGGLN NLFK L+++K+W ++++ +L LIGS
 Sbjct: 61 LEYKHPYLEERETKRVGYLVVSTDRGLCGGLNTNLFKKLLSEMKDWSKDQVQCELALIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K SFF S G N+ Q++G+GD P+L ELIG N M AY G +D +Y+ NKF+NTMS
 Sbjct: 121 KATSFFASVGGNVVAQVTGMGDNPSLSELIGPVNIMLRAYDEGRDLKLYVVTNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q+P + QL+PLP D+ L ++++WDYLYEP+PK LLD LL RY+ESQ+YQ VV+N+AS
 Sbjct: 181 QEPTITQLLPLPAGDDETL--KKKSWDYLYEPDPKALLDILLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GA+A+
 Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGASAV 287

tr Q8E8B9 **ATP synthase F1, gamma subunit [ATPG] [Shewanella oneidensis]** 286 AA
align

Score = 385 bits (990), Expect = e-106
 Identities = 183/289 (63%), Positives = 237/289 (81%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEIKTKIASV++TQKIT AMEMVA SKMR+ Q+RMAASRPY+E++R VI HV++ S
 Sbjct: 1 MAGAKEIKTKIASVKNTQKITSAMEMVAASKMRRQAQERMAASRPYAESMRKVIGHVAQGS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKHP+L RE K++G +V++TDRG+CGGLNVNLFK + +K+WKEQ + IG+
 Sbjct: 61 LEYKHPYLEVREAKRVGYIVVATDRGLCGGLNVNLFKKVVADVKSWEQGAEFEFCPIGA 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 + + FF+SFG + Q SGLGD P L +LIG M +AY G++D +Y+ +NKFVNTM+
 Sbjct: 121 RSVQFFKSFGGQVSAQASGLGDAPKLNLDLIGTVQVMLEAYNEGKLDRLYVVFNKFVNTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q PV++QL+PLP+S+DD + R WDY+YEP+PK LLD+LLVRY+ESQ+YQ VV+N+AS
 Sbjct: 181 QTPVIEQLLPLPKSEDDEVAHR---WDYIYEPDPKALLDILLVRYVESQVYQGVVENIAS 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARMVAMKAATDNAG LI+DL+LVYNKARQA+IT EL+EIV+GA+A+
 Sbjct: 238 EQAARMVAMKAATDNAGTLIDDLQLVYNKARQAAITQELSEIVSGASAV 286

tr Q8Z2Q5 **ATP synthase gamma subunit [STY3912] [Salmonella typhi]** 287 AA
align

Score = 385 bits (989), Expect = e-106

Identities = 187/289 (64%), Positives = 235/289 (80%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+QDRMAASRPY+ET+R VI H++ +
 Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLANGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKHP+L ER+VK++G LV+STD G+CGGLN+NLFK L +K W ++ + +L +IGS
 Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDCGLCGGLNINLFFKLLADMKAWSKGVQCELAMIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 KG+SFF S G N+ Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
 Sbjct: 121 KGVSFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRDLKLYIVSNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q P + QL+PLP S+DD L ++ WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS
 Sbjct: 181 QVPTITQLLPLPASEDDDL--KRTAWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV+GAAA+
 Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVSGAAAV 287

tr Q8Z9S5 **ATP synthase gamma subunit protein (EC 3.6.1.34) (Membrane-bound ATP synthase, F1 sector, gamma-subunit) [ATPG] [Yersinia pestis]** 287 AA
align

Score = 381 bits (979), Expect = e-105

Identities = 186/289 (64%), Positives = 236/289 (81%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEI++KIASVQ+TQKITKAMEMVA SKMRK+Q+RMAASRPY+ET+R+VI H++ +
 Sbjct: 1 MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQERMAASRPYAETMRSVIGHLALGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKHP+L ER+VK++G LV+STD RG+CGGLN+NLFK L ++K W E+ + DL LIGS
 Sbjct: 61 LEYKHPYLEERDVKRVGYLVVSTDRGLCGGLNINLFFKRLLAEMKGWSEKGVVECDLALIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K SFF S G I Q++G+GD P+L ELIG M AY G +D +YI NKF+NTMS
 Sbjct: 121 KAASFFGSVGGKIVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRDLKLYIVNNKFINTMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q+P + QL+PLP ++D L ++++WDYLYEP+PK LLD+LL RY+ESQ+YQ VV+N+AS

Sbjct: 181 QEPRIMQLLPLPPAEDGEL--KKKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDN G+LI +L+LVYNKARQASIT EL EIV GA+A+

Sbjct: 239 EQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEIVGGASAV 287

tr Q9KNH4 **ATP synthase F1, gamma subunit [VC2765] [Vibrio cholerae]** 288 AA

align

Score = 376 bits (965), Expect = e-103

Identities = 179/289 (61%), Positives = 233/289 (79%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI+TKI SV+STQKITKAMEMVA SKMR++QD M +SRPY++TIR VI HV+ AS

Sbjct: 1 MAGAKEIRTKIGSVKSTQKITKAMEMVAASKMRRSQDAMESSRPYAQTIRKVIGHVANAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+HP+L ERE K++G ++ISTDRG+CGGLN+NLFK + ++ WKE+ +L +IGS

Sbjct: 61 LEYRHPYLEEREAKRVGYIIISTDRGLCGGLNINLFFKAITDMQTWKEKGAQIELAIIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K +FF + G + Q+SGLGD+P+LE+LIG M Y GE+D +Y+ +N+FVNTM

Sbjct: 121 KATAFFNNSGAKVAAQVSGLGDSPLSDLIGSVGVMLKKYDKGELDRLYLVFNQFVNTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
QKP + QL+PLP+S + + +R WDY+YEPEPK LLD+LL+R++ESQ+YQ VV+N+A

Sbjct: 181 QKPKIDQLLPLPKSDSEDM-QRDHMDYIYEPEPKPLLDALLLRFIESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNA NLI+DL+LVYNKARQA+IT EL+EIV GAAA+

Sbjct: 240 EQAARMVAMKAATDNASNLIDDLQLVYNKARQAAITQELSEIVGGAAAV 288

tr Q7MGH9 **F0F1-type ATP synthase, gamma subunit [VV3252] [Vibrio** 288
vulnificus AA
(strain YJ016)] align

Score = 375 bits (964), Expect = e-103

Identities = 180/289 (62%), Positives = 235/289 (81%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ AS

Sbjct: 1 MAGAKEIRSKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+HP+L ERE K++G ++ISTDRG+CGGLN+N+FK + ++ WKE+ +L +IGS

Sbjct: 61 LEYRHPYLDEREAKRVGYIIISTDRGLCGGLNINVFKAVTDMQAWKEKGAEVELAVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K +FF+ G + Q+SGLGD+P+LE+LIG + M + Y GE+D +Y+ +NKFVNTM

Sbjct: 121 KATAFFKHGGAKVAAQVSGLGDSPLSDLIGSVSVMLEKYDEGELDRLYLVFNKFNVTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240

Q+P + QL+PLP+S D +R+ +WDY+YEPEP+ LLD+LLVRY+ESQ+YQ VV+N+A
Sbjct: 181 QQPTIDQLLPLPKS-DSKDMQREHSWDYIYEPEPQALLDALLVRYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+
Sbjct: 240 EQAARMVAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288

tr Q8DDG9 **ATP synthase F1, gamma subunit [VV11020] [Vibrio vulnificus]** 288 AA

align

Score = 375 bits (964), Expect = e-103
Identities = 180/289 (62%), Positives = 235/289 (81%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ AS
Sbjct: 1 MAGAKEIRSKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+HP+L ERE K++G ++ISTDRG+CGGLN+N+FK + ++ WKE+ +L +IGS
Sbjct: 61 LEYRHPYLDEREAKRVGYIIISTDRGLCGGLNINVFKKAVTDMQAWKEKGAEVELAVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K +FF+ G + Q+SGLGD+P+LE+LIG + M + Y GE+D +Y+ +NKFVNTM
Sbjct: 121 KATAFFKHGGAKVAAQVSGGLDPSLEDLIGSVSVMLEKYDEGELDRLYLVFNKFNVTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
Q+P + QL+PLP+S D +R+ +WDY+YEPEP+ LLD+LLVRY+ESQ+YQ VV+N+A
Sbjct: 181 QQPTIDQLLPLPKS-DSKDMQREHSWDYIYEPEPQALLDALLVRYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARMVAMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+
Sbjct: 240 EQAARMVAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288

tr Q87KA7 **ATP synthase F1, gamma subunit [VP3070] [Vibrio** 288
parahaemolyticus] AA

align

Score = 374 bits (959), Expect = e-102
Identities = 178/289 (61%), Positives = 231/289 (79%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI+ KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ A+
Sbjct: 1 MAGAKEIRNKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+HP+L ERE K++G +++STDRG+CGGLN+N+FK + I+ WKE+ +L +IGS
Sbjct: 61 LEYRHPYLEEREAKRVGYIIVSTDRGLCGGLNINVFKKAVTDIQTWKEKGAEIELAVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K +FF+ G + Q+SGLGD+P+LE+LIG M Y GE+D +Y+ +NKFVNTM
Sbjct: 121 KATAFFKHGGAKVAAQVSGGLDPSLEDLIGSVGVMLKKYDEGELDRLYVVFNKFVNTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
 Q+P + QL+PLP+S D +R+ +WDY+YEPEPK LLD+LLVRY+ESQ+YQ VV+N+A
 Sbjct: 181 QQPTIDQLLPLPKS-DSKEMQREHSWDYIYEPEPKPLDRTLVRVYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARM+AMKAATDNA NLI DL LVYNKARQA+IT EL+EIV GA+A+
 Sbjct: 240 EQAARMIAMKAATDNATNLIEDLELVYNKARQAAITQELSEIVGGASAV 288

sp P12990 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Vibrio 288 AA**
ATPG_VIBAL alginolyticus]

align

Score = 373 bits (958), Expect = e-102

Identities = 175/289 (60%), Positives = 232/289 (79%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEI+ KI SV+STQKITKAMEMVA SKMR++QD M ASRPY+ET+R VI HV+ A+
 Sbjct: 1 MAGAKEIRNKIGSVKSTQKITKAMEMVAASKMRRSQDAMEASRPYAETMRKVIGHVANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + Y+HP+L ERE K++G +++STDRG+CGGLN+N+FK + ++ W+E+ +L ++GS
 Sbjct: 61 LEYRHPYLEEREAKRVGYIIVSTDRGLCGGLNINVFKKAVTDMQWREKGAEIELAVVGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K +FF+ G + Q+SGLGD P+LE+LIG M Y GE+D +Y+ +NKFVNTM
 Sbjct: 121 KATAFFKHGGAKVAAQVSGLDNPSLEDLIGSVGVMLKKYDEGELDRLYVVFNKFVNTMV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
 Q+P + QL+PLP+S + + +R+ +WDY+YEPEPK LLD+LLVRY+ESQ+YQ VV+N+A
 Sbjct: 181 QQPTIDQLLPLPKSDSEEM-QREHSWDYIYEPEPKPLDRTLVRVYVESQVYQGVVENLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARM+AMKAATDNA NLI+DL LVYNKARQA+IT EL+EIV GAAA+
 Sbjct: 240 EQAARMIAMKAATDNATNLIDDLELVYNKARQAAITQELSEIVGGAAAV 288

tr Q9HT19 **ATP synthase gamma chain [ATPG] [Pseudomonas 286 AA**
aeruginosa] align

Score = 362 bits (928), Expect = 5e-99

Identities = 178/289 (61%), Positives = 225/289 (77%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAA RPY+E IR VI H++ A+
 Sbjct: 1 MAGAKEIRSKIASIKSTQKITNAMEKVAVSKMRKAQMRMAAGRPAERIRQVIGHLANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 Y+HPF+VEREVK++G +V+S+DRG+CGGLN+NLFK+ + + ++EQ DL +IGS
 Sbjct: 61 PEYRHPFMVEREVKRVGYIIVSSDRGLCGGLNINLFKSLVKDMSGYREQGAEIDLVCVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 KG SFFRSFG N+ +S LG+ P++ +LIG M DAY G ID +++ NKFVNTM+
 Sbjct: 121 KGASFFRSFGGNVVAISHLGEEPSINDLIGSVKVMLDAYLEGRIDRLFVVSNNKFVNTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
QKP V+QL+PL D L WDYLYEP+ K LLD LLVRY+ESQ+YQAVV+N A
Sbjct: 181 QKPTVEQLIPLVADDDQELKHH---WDYLYEPDAKSLLDGLLVRYVESQVYQAVVENNAC 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARM+AMK ATDNAG LI+DL+L+YNKARQA+IT E++EIV GAAA+
Sbjct: 238 EQAARMIAMKNATDNAGELISDLQLIYNKARQAAITQEISEIVGGAAAV 286

tr Q8VV78 **F0F1-ATPase subunit gamma [ATPG] [Colwellia maris (Vibrio sp. 287 AA
(strain ABE-1))]**

align

Score = 353 bits (906), Expect = 2e-96

Identities = 171/289 (59%), Positives = 223/289 (76%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA KEIKTKIASV+ TQKIT AMEMVA SKMRK Q+ MAASRPY+ IRNVI H++ +
Sbjct: 1 MAVGKEIKTKIASVKGTQKITSAMEMVAASKMRKAQEGMAASRPYATNIRNVIGHIALGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+HP++ ERE K++G +V+S+DRG+CGGLN+NLFK L + + +IGS
Sbjct: 61 LEYRHPYMDEREAKRVGYIVVSSDRGLCGGLNINLFKKVLADAAEKQASGAEEVEFCVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
K +FF + G + Q+SGLGD+P+L +L+G M AY NGEID +++ YNKFVNTM+
Sbjct: 121 KATAFFNNMGAKVSAQISGLGDSPLSLDVLGVSVAVMLKAYDNGEIDRLHVVYNKFVNTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
Q+P + QL+PLP+S D+ ++ R WDY+YEP+ LLD LLVRY+ESQ+YQ VV+N+A
Sbjct: 181 QEPTIDQLLPLPKSDDEAISHR---WDYIYEPDANSLLDQLLVRYIESQVYQGVVENIAC 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQA+RMV+MKAATDNAG+LI+DL+LVYNKARQA+IT EL EIVAGAAA+
Sbjct: 238 EQASRMVSMKAATDNAGDLIDDLQLVYNKARQAAITQELGEIVAGAAAV 286

tr Q88BX3 **ATP synthase F1, gamma subunit [ATPG] [Pseudomonas putida 286
(strain AA
KT2440)]**

align

Score = 349 bits (896), Expect = 2e-95

Identities = 173/289 (59%), Positives = 223/289 (76%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAASRPY+E IR VI H++ A+
Sbjct: 1 MAGAKEIRSKIASIKSTQKITSAMEKVAVSKMRKAQMRMAASRPYAERIRQVIGHLANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
Y+HPF++ER VK+ G +V+S+DRG+CGGLN NLFK + + +EQ + DL +IGS
Sbjct: 61 PEYRHPFMIERPVKRAGYIVVSSDRGLCGGLNTNLFKALVKDMSANREQGVEIDLVCVIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG +FFR FG N+ +S LG+ P++ +LIG M DAY +G ID + + NKF+NTM+
Sbjct: 121 KGATFFRIFGNGVVAASHLGEEPSINDLIGSVKVMLDAYLDGRIDRLSVVSNKFINTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
QKP V+QLVPL + D L WDYLYEP+ K LLD L+VRY+ESQ+YQAVV+N A+
Sbjct: 181 QKPTVEQLVPLVATPDQDLKHH---WDYLYEPDAKELLDGLMVRYVESQVYQAVVENNAA 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARM+AMK ATDNAG+LI +L+L+YNKARQA+IT E++EIV GAAA+
Sbjct: 238 EQAARMIAMKNATDNAGDLIKELQLIYNKARQAAITQEISEIVGGAAAV 286

tr Q87TT3 **ATP synthase F1, gamma subunit [ATPG] [Pseudomonas syringae** 286
(pv.
tomato)] AA
align

Score = 347 bits (891), Expect = 9e-95
Identities = 170/289 (58%), Positives = 225/289 (77%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAGAKEI++KIAS++STQKIT AME VA SKMRK Q RMAASRPY+E IR VI H++ A+
Sbjct: 1 MAGAKEIRSKIASIKSTQKITSAMEKVAVSKMRKAQMRMAASRPYAERIRQVIGHLANAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
Y HPF++ER +K++G +V+S+DRG+CGGLN NLFKT + + +E + DL ++GS
Sbjct: 61 PEYLHPFMIERPLKRVGYVVVSSDRGLCGGLNTNLFKTLVKDMAVNRENGVEIDL CVVG 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNK FVNTMS 180
KG +FFR+FG N+ +S LG+ P++ +LIG M DAY +G ID + + NKF+NTM+
Sbjct: 121 KGAAFFRNFGGNVVAISHLGEEPSINDLIGSVKVMLDAYLDGRIDRLSVVSNKFINTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
Q+P V+QL+PL + D L WDYLYEP+ K LLD L+VRY+ESQ+YQAVV+N A+
Sbjct: 181 QQPTVEQLIPLVATPDQGLKHH---WDYLYEPDAKELLDGLMVRYVESQVYQAVVENNAA 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
EQAARM+AMK ATDNAG+LI+DL+L+YNKARQA+IT E++EIV GAAA+
Sbjct: 238 EQAARMIAMKNATDNAGDLISDLQLIYNKARQAAITQEISEIVGGAAAV 286

tr Q83AF6 **ATP synthase, F1 gamma subunit [ATPG] [Coxiella burnetii]** 289 AA
align

Score = 338 bits (868), Expect = 4e-92
Identities = 169/291 (58%), Positives = 223/291 (76%), Gaps = 5/291 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
M+ A+EI+TKIAS+++TQKIT+AME+VA SKMRK QDRMA SRPY+ IR VISHV+ +
Sbjct: 1 MSKAREIRT KIASIKNTQKITRAMELVAA SKMRKAQDRMAMSRPYASKIRKVISHVAASH 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
Y HP+L +RE +K++G ++++TDRG+CGGLNVNLF+T + +K W+ NI DL +IG
Sbjct: 61 AEYHPHYLQQRENIRKRVGYIIVTTDRGLCGGLNVNLFRTAIDMKKWQADNIGMDLCVIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNK FVNTM 179
KG +FFR +G N+ LGD P ++++IG+ M D Y +IDA+YIA N+ FVNTM

Sbjct: 121 RKGEAFFRRYGGNVLAHADHLDGDAPEVQDIIGIVKVMLDQYDKQQIDAIYIATNEFVNTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEP-EPKVLLDSLLVRYLESQIYQAVVDNV 238
 QKP+V+QL+PL K D WDY+YEP E K LL+ LLVRY+ESQ+YQAV++N+

Sbjct: 181 VQKPLVRQLLPL---KTDEEEVEGGYWDYIYEPDESKDLLEMLLVRYIESQVYQAVIENI 237

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 A EQ+ARMVAMK AT+NAG LI++LRL+YNKARQA IT E+ EIVAGAAA+

Sbjct: 238 ACEQSARMVAMKNATENAGQLIDELRLIYNKARQAGITREIAEIVAGAAAV 288

tr Q82XP9 **ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Nitrosomonas europaea]** 294 AA

align

Score = 337 bits (865), Expect = 1e-91

Identities = 159/294 (54%), Positives = 222/294 (75%), Gaps = 5/294 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M ++EI+ KI SV++TQKIT+AMEMVA SKMRK QDRM +RPY E IRNV +H+S AS

Sbjct: 1 MPSSREIRNKKISVKNTQKITRAMEMVAASKMRKAQDRMKKARPYGEKIRNVAAHMSNAS 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 + Y+HPFL+ R+ VK++GI+V+++D+G+CGGLN N+ + LN+I+ W+ + D IG

Sbjct: 61 VEYRHPFLISRDSVKRVGIIIVVTSKGLCGGLNTNVLRALNEIRTWETEGNHVDACCIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKVFNTM 179
 +KG+ F G + Q++GLGD P +E LIG + DAY G++D VYI YN+F+NTM

Sbjct: 121 NKGLGFMSRLGTQVISQVTGLGDAPNMERLIGAVKVVLDAYTEGQLDRVYIFYNRFINTM 180

Query: 180 SQKPVVQQLVPLPE---SKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235
 Q PV++QL+PL + S+D + WDY+YEPE K ++D ++VRY+E+ +YQAV

Sbjct: 181 KQMPVMEQLLPLTDDRISSEGEARPTAPWDYIYEPEAKPVIDDIMVRYIEALVYQAVA 240

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +N+ASEQ+ARMVAMKAA+DNAGNLI++L L+YNK+RQA+IT EL+EIV GAAA+

Sbjct: 241 ENMASEQSARMVAMKAASDNAGNLIDELTLIYNKSRQAATKELSEIVGGAAAV 294

tr Q8XU75 **Probable ATP synthase gamma chain protein (EC 3.6.1.34) [ATPG] 291 AA**
[Ralstonia solanacearum (Pseudomonas solanacearum)]

align

Score = 331 bits (848), Expect = 9e-90

Identities = 158/291 (54%), Positives = 223/291 (76%), Gaps = 2/291 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAG KEI+TKI SVQ+T+KITKAMEMVA SKMR+ Q+RM ++RPY+E IRNV +H+++A+

Sbjct: 1 MAGTKEIRTKIKSVQNTKTKITKAMEMVAASKMRRAQERMRSARPYAEKIRNVAAHMAQAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 Y+HPF+V+R+VK+ G++V++TD+G+CGGLN N+ + NQ+++ + + + + IGS

Sbjct: 61 PEYQHPFMVKRDVKRAGLIVVTTDKGLCGGLNTNVLRVAVTNQLRDLQNKGVESQATAIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKVFNTMS 180

KG+ F G + + LGDTP LE+LIG DA+ GEIDAVY+AY +F+NTM
 Sbjct: 121 KGMQFLGRIGAKVVSNNVHLGDTPLHLEKLIGAIVQLDAFTAGEIDAVYLAYTRFINTR 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQ--TWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNV 238
 Q+PVV+QL+PL K +Q +WDY+YEP+ + ++D LL+RY+E+ +YQAV +N+
 Sbjct: 181 QEPVVEQLLPLTADKLTQTAAEKQAYSWDYIYEPDAQTVVDELLIRYVEALVYQAVAENM 240

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 ASEQ+ARMVAMKAA+DNA N+I +L+LVYNK RQA+IT EL+EIV GAAA+
 Sbjct: 241 ASEQSARMVAMKAASDNAKNVIGELQLVYNKTRQAAITKELSEIVGGAAAV 291

tr Q8PCZ6 **ATP synthase gamma chain [ATPG] [Xanthomonas campestris (pv. 287 AA
 campestris)]**

align

Score = 323 bits (827), Expect = 2e-87

Identities = 155/290 (53%), Positives = 220/290 (75%), Gaps = 4/290 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAG +EIKTKI SVQ+T+K+T+A+EMV+ SK+RK Q+RM SRPY++ ++ VI H+++AS
 Sbjct: 1 MAGGREIKTKIKSVQNTKRVTRALEMVSASKIRKAQERMKTSRPYAQAMKQVIGHLAQAS 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 Y+HPFLVERE VK++G +VIS+DRG+ GGLN NLF+ L +++ W+++ D+ IG
 Sbjct: 61 TDYQHPFLVEREQVKRVGYIVISSDRGLAGGLNNNLFKMLGEVRPWQDKGAEIDVVTIG 120

Query: 120 SKGISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
 K +FFR N+ G ++ LGD+P +E+L+GV M DA+ G++D VY+ YN+FVNTM
 Sbjct: 121 QKASAFFRRIKVNMGVSVTHLGDSPHIEQLVGVIVKMLDAFTEGKVDRVYLVYNRFVNTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVA 239
 +QK +QL+PLP ++ WDYLYEP+ +L+ ++ RY+ES +YQAV++NVA
 Sbjct: 181 TQKASFEQLLPLPAAEH---KVAHHDWDYLYEPDAATVLEHVMTRYIESLVYQAVLENVA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 SE AARMVAMKAA+DNA +I L+LVYNKARQA+IT E++EIV+GAAA+
 Sbjct: 238 SEHAARMVAMKAASDNANKMIGTLQLVYNKARQAAITQEISEIVSGAAAV 287

sp O51873 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera 291
 ATPG_BUCAP aphidicola AA
 (subsp. Schizaphis graminum)]** align

Score = 322 bits (826), Expect = 3e-87

Identities = 162/289 (56%), Positives = 218/289 (75%), Gaps = 1/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA KEIK +I SV +T+KITKAMEMVA SKMRKT++RM RPYSE I+ VI HV + S
 Sbjct: 1 MASKKEIKDQIISVTNTKKITKAMEMVAVSKMRKTEERMRLGRPYSEIHKVIHHLVQGS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKH +L +R K+IGI+++STDRG+CG LN NLFK L +I+N+ + NI DL L G
 Sbjct: 61 LEYKHSYLEKRNDKRIGIIVSTDRGLCGSLNTNLFKQVLFKIQNFAKINIPCDLILFGL 120

Query: 121 KGISFFRSFGFNKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K +S F+ +G +I ++ LG+TP L +LIG + + Y+N +ID ++IAYNKF N +S
 Sbjct: 121 KLSLVFKLYGSSIISSVTNLGETPDLSKLIGSIKIILEKYQNNQIDRLFIAYNKFHNKLS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q P + QL+PL K+ N++ + WDYLYEPE K++LD+L RY+ESQIYQ++++N+AS
 Sbjct: 181 QYPKISQLLPLYNEKNIFSNNKIK-WDYLYEPESKLILDTLFDRYIESQIYQSLLENIAS 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQAARMVAMK ATDN+GN I +L+L+YNK RQA+IT EL EIVAGA+A+
 Sbjct: 240 EQAARMVAMKTATDNSGNRIKELQLIYNKVRQANITQELTEIVAGASAV 288

sp P57123 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera** 290
 ATPG_BUCAI **aphidicola** AA
 (subsp. *Acyrtosiphon pisum*) (*Acyrtosiphon pisum* align
 symbiotic bacterium)]

Score = 322 bits (826), Expect = 3e-87

Identities = 161/289 (55%), Positives = 212/289 (72%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M KEIK KI SV +T+KITKAMEMVA SKMRKT++RM + RPYS+ IR VI HV++ +
 Sbjct: 1 MTSTKEIKNKIVSVTNTKKITKAMEMVAVSKMRKTEERMRSRGPYSIDIIRKVIDHVTQGN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKH +L ER+ +IG+++ISTDRG+CGGLN NLFK L +I+N+ + NI DL L G
 Sbjct: 61 LEYKHSYLEERKTNRIGMIIISTDRGLCGGLNTNLFKQVLFKIQNFAKVNIPCDLILFGL 120

Query: 121 KGISFFRSFGFNKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K +S F+ G NI + + LG+ P LEELI + Y+ ID ++IAYNKF N MS
 Sbjct: 121 KLSLVFKLCGSNILAKATNLGENPKLEELINSVGIIILQEYQCKRIDKIFIAYNKFHNKMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q P + QL LP SK + + WDYLYEPE K++LD+L RY+ESQ+YQ++++N+AS
 Sbjct: 181 QYPTITQL--LPFSKKNQDASNNNWDYLYEPESKLILDTLFNRYIESQVYQSILENIAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E AARM+AMK ATDN+GN I +L+LVYNK RQA+IT ELNEIV+GA+A+
 Sbjct: 239 EHAARMIAMKTATDNSGNRIKELQLVYNKVRQANITQELNEIVSGASAV 287

tr Q8PGG6 **ATP synthase gamma chain [ATPG] [*Xanthomonas axonopodis* (pv. citri)]** 287 AA
align

Score = 318 bits (816), Expect = 5e-86

Identities = 154/290 (53%), Positives = 219/290 (75%), Gaps = 4/290 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MAG +EIKTKI SVQ+T+K+T+A+EMV+ SK+RK Q+RM SRPY++ ++ VI H+++AS
 Sbjct: 1 MAGGREIKTKIKSVQNTKRVTRALEMVSASKIRKAQERMKTSRPPYAQAMKQVIGHLAQAS 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 ++HPFL+ERE VK++G +VIS+DRG+ GGLN NLF+ L +++ W+++ D+ IG

Sbjct: 61 TDFQHPFLIEREQVKRVGYIVISSDRGLAGGLNNNLFRKMLGEVRPWQDKGAEIDVVTIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKVFNTM 179
 K +FFR N+ G ++ LGD+P +E+LIGV M DA+ G++D VY+ YN+FVNTM

Sbjct: 121 QKASAFFRRVKVNMVGSVTHLGDSPQVEQLIGVIKVMIDAFIEGKVDRVYLVYNRFVNTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
 +QK QL+PLP ++ WDYLYEP+ +L+ ++ RY+ES +YQAV++NVA

Sbjct: 181 TQKASFDQLLPLPAAEH---KVAHHDWDYLYEPDAASVLEHVMTRYIESLVYQAVLENVA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 SE AARMVAMKAA+DNA +I L+LVYNKARQA+IT E++EIV+GAAA+

Sbjct: 238 SEHAARMVAMKAASDNANKMIGTLQLVYNKARQAAITQEISEIVSGAAAV 287

tr Q87E89 **ATP synthase gamma chain [ATPG] [Xylella fastidiosa (strain 287 AA
 Temecula1 / ATCC 700964)]**

align

Score = 305 bits (781), Expect = 5e-82

Identities = 150/290 (51%), Positives = 209/290 (71%), Gaps = 4/290 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA +EIK+KI SVQ+T+K+T+A+EMV+ SK+RK Q++M SRPY++ ++ +I H+++A+

Sbjct: 1 MASGREIKSKIKSQVQNTKRVTRALEMVSASKIRKAQEQMKISRPYAQAMQMIGHLAQAN 60

Query: 61 IGYKHPFLV-EREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 Y HPFL+ ++VK+IG +VIS+DRG+ GGLN NLF+ L ++ W++ D+ IG

Sbjct: 61 TEYLHPFLIAHKQVKRIGYIVISSDRGLAGGLNNNLFRKMLGEMHQWQDNGAEVDIVTIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKVFNTM 179
 K FFR NI G ++ LGDTP LE+LIGV M DAY ++D VY+ YN F+NTM

Sbjct: 121 QKASVFFRRIKVNILGSVTHLGDTPRLEQLIGVIKVMMLDAYTEEKLDREVYLVYNHFINTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
 QK QL+PL +KD WDYLYEP+ +L+ ++ RY+ES +YQA+++N+A

Sbjct: 181 VQKASFDQLLPLLAAKD---KVAHHDWDYLYEPDAATVLEHVMTRYIESLVYQAMLENIA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 SE AARMVAMKAA+DNA LI L+LVYNKARQA+IT E++EIV GAAA+

Sbjct: 238 SEHAARMVAMKAASDNANKLIGTLQLVYNKARQAAITQEISEIVGGAAAV 287

tr Q9PE84 **ATP synthase, gamma chain [XF1144] [Xylella fastidiosa]** 287 AA
align

Score = 305 bits (781), Expect = 5e-82

Identities = 149/290 (51%), Positives = 211/290 (72%), Gaps = 4/290 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA +EIK+KI SVQ+T+K+T+A+EMV+ SK+RK Q++M SRPY++ ++ + H+++A+

Sbjct: 1 MASGREIKSKIKSQVQNTKRVTRALEMVSASKIRKAQEQMKISRPYAQAMQMIGHLAQAN 60

Query: 61 IGYKHPFLV-EREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 Y HPFL+ ++VK+IG +VIS+DRG+ GGLN NLF+ L +++ W+++ D+ IG

Sbjct: 61 TDYLHPFLIAHKQVKRIGYIVISSDRGLAGGLNNNLFRKMLGEMRQWQDKGAEVDIVTIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
 K FFR NI G ++ LGDTP LE+LIGV M DAY ++D VY+ YN+F+NTM

Sbjct: 121 QKASVFFRRIKVNILGSVTHLGDTPRLEQLIGVIKVMLDAYTEEKLDREVYLVYNRFINTM 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 239
 QK QL+PL +KD WDYLYEP+ +L+ ++ RY+ES +YQAAA+N+A

Sbjct: 181 VQKASFDQLLPLLAAKD---KVAHHDWDYLYEPDAATVLEHVMRRYIESLVYQAMLENIA 237

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 SE AARMVAMKAA+DNA LI L+LVYNKARQA+IT E++EIV GAAA+

Sbjct: 238 SEHAARMVAMKAASDNANKLIGTLQLVYNKARQAAITQEISEIVGGAAAV 287

tr Q7VU45 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA
 pertussis]**

align

Score = 304 bits (779), Expect = 9e-82

Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+ +R + +H+ +A+

Sbjct: 1 MPGIKEIRTKIKSVQNTKTKITKAMEMVAASKMRKAQERMAGRPHYATKVREIAAHLMQAN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++I G+

Sbjct: 61 PEYSHPYLVEREVKAVGVVLVTTDKGLCGGLNTNISRVTL SKLKEFEQRSIKVQATAFGN 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 KG+ G + Q LGD P L+ L+G D Y G IDA+Y+A +FVNTM

Sbjct: 121 KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMK 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQT-----WDYLYEPEPKVLLDSLLVRYLES 228
 Q+PV +L+PL DD +T WDY+YEP+ K ++D LL RY+E

Sbjct: 181 QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240

Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
 +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA

Sbjct: 241 LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300

Query: 289 I 289
 +

Sbjct: 301 V 301

tr Q7WEM8 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA
 bronchiseptica (Alcaligenes bronchisepticus)]**

align

Score = 304 bits (778), Expect = 1e-81

Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60

```
      M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+  +R + +H+ +A+
Sbjct: 1  MPGIKEIRTKIKSVQNTKTKITKAMEMVAASKMRKAQERMRAGRPYATKVREIAAHLMQAN 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
      Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++I      G+
Sbjct: 61  PEYSHPYLVEREVKAVGVVLVTTDKGLCGGLNTNISRVTLTKLKEFEQRSIKVQATAFGN 120

Query: 121  KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
      KG+      G + Q   LGD P L+ L+G      D Y G IDA+Y+A +FVNTM
Sbjct: 121  KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMR 180

Query: 181  QKPVVQQLVPLPESKDDHLNERQQT-----WDYLYEPEPKVLLDSLLVRYLES 228
      Q+PV  +L+PL   DD      +T      WDY+YEP+ K ++D LL RY+E
Sbjct: 181  QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240

Query: 229  QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
      +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA
Sbjct: 241  LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300

Query: 289  I 289
      +
Sbjct: 301  V 301
```

tr Q7W3A9 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bordetella 301 AA
parapertussis]**

align

Score = 303 bits (776), Expect = 2e-81

Identities = 149/301 (49%), Positives = 208/301 (68%), Gaps = 12/301 (3%)

```
Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
      M G KEI+TKI SVQ+T+KITKAMEMVA SKMRK Q+RM A RPY+  +R + +H+ +A+
Sbjct: 1  MPGIKEIRTKIKSVQNTKTKITKAMEMVAASKMRKAQERMRAGRPYATKVREIAAHLMQAN 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
      Y HP+LVEREVK +G+++++TD+G+CGGLN N+ + TL+++K +++++I      G+
Sbjct: 61  PEYGHYPYLVVEREVKAVGVVLVTTDKGLCGGLNTNISRVTLTKLKEFEQRSIKVQATAFGN 120

Query: 121  KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
      KG+      G + Q   LGD P L+ L+G      D Y G IDA+Y+A +FVNTM
Sbjct: 121  KGLGLLTRIGAKLVSQEVQLGDKPDLDRLLGAIKVQLDDYLEGRIDALYVATTRFVNTMR 180

Query: 181  QKPVVQQLVPLPESKDDHLNERQQT-----WDYLYEPEPKVLLDSLLVRYLES 228
      Q+PV  +L+PL   DD      +T      WDY+YEP+ K ++D LL RY+E
Sbjct: 181  QEPVFLRLLPLSNGLDDPFQSGVETLAKTAEIKSDYSWDYIYEPDAKSVIDDLLQRYVEG 240

Query: 229  QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
      +YQAV +N+ASEQ+ARMVAMK+A+DNA +I DL+LVYNK RQA+IT E++EIV GAAA
Sbjct: 241  LLYQAVAENMASEQSARMVAMKSASDNAKKVIGDLQLVYNKTRQAAITKEISEIVGGAAA 300

Query: 289  I 289
      +
Sbjct: 301  V 301
```

tr Q7VQV7 **ATP synthase gamma subunit (EC 3.6.3.14) [ATPG] [Candidatus Blochmannia floridanus]** 288 AA

align

Score = 302 bits (774), Expect = 3e-81

Identities = 147/291 (50%), Positives = 209/291 (71%), Gaps = 5/291 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
M+ KE++ KI S+++ QK++KAMEM+A SKM+K Q M S+PY++ IR VI H+S
Sbjct: 1 MSSIKEVREKIESIRNIQKLSKAMEMIAASKMKKAQRLMLVSQPYTKAIRKVIDHISLGK 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+ Y+H +L+ REV+ +G VIS+DRG+ GGLNVN+F+ LN I W + N++ L +IGS
Sbjct: 61 LEYRHVYLMNREVRVSVGYWVISSDRGLAGGLNVNVRMLLNDISRWNKLNVTIKLAIIGS 120

Query: 121 KGISFFRSFGFN-IKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
K ISFF N I +SG+GD P + +LIG+ TM Y NG++D +Y+ YNKF+NT+
Sbjct: 121 KAISFFNCIDPNMIVSVYSGIGDVPKMSQLIGLVGTMLQLYCNGQVDRLYLIYNKFINTL 180

Query: 180 SQKPVVQQVLVPL-PESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNV 238
SQ P + Q++P+ ES + + + WDYLYEP+ KVLDD+LL RY+ESQ+YQ VV+N+
Sbjct: 181 SQVPKIIQILPIFSESNNTCVTKH--WDYLYEPDSKVLLDTLLNRYIESQVYQGVVENL 237

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
ASEQ+ARM+AMK A+DN +I DLR+ YNK RQ+ IT EL EI++G++ I
Sbjct: 238 ASEQSARMIAMKTASDNGETI IKDLRVFYNKLRQSKITQELAEIISGSSVI 288

sp P41169 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG]** 298
ATPG_THIFE **[Thiobacillus ferrooxidans]** AA
align

Score = 301 bits (771), Expect = 8e-81

Identities = 144/287 (50%), Positives = 213/287 (74%), Gaps = 1/287 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA AKEI+ +I SV++T+KIT+AMEMVA SKMR+ Q+RM A+RP +E IR V+ H+++A
Sbjct: 1 MANAKEIRGQIKSVKNTRKITRAMEMVAASKMRRAQERMRAARPCA EKIREVLGHLAQAH 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
Y+HP + R VKK G LV++TDRG+CGGLNVN+ + + +++ E+ + ++L ++G+
Sbjct: 61 PEYEHPLMQVRPVKKAGFLVVTDRGLCGGLNVNVLNRNVVQKMRELHEEGVESNLAVVGN 120

Query: 121 KGISFFRSFGFNKIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG+ F R G ++ ++GLGD+P L ++IG M DAY GE+D VY+ ++FVNTM
Sbjct: 121 KGLGFLRRHGAHLVADVNGLGDSPLGDMIGPIRAMADAYAKGEVDVVYLSSRFVNTML 180

Query: 181 QKPVVQQVLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVAS 240
Q+ V+QL+P+ E +R + WDY+YEPE + +LD L+ RY+ES +YQAV++++A
Sbjct: 181 QRATVEQLLPV-EKPTASAEQRAELWDYIYEPEARPVLDRLMQRYVESVYQAVIEHLAC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAA 287
EQ+ARMVAMK+A+DNA +++DL+L YNKARQA+IT E+ EI AGAA
Sbjct: 240 EQSARMVAMKSASDNAKRMVDDLQLAYNKARQAAITQEIAEISAGAA 286

Score = 300 bits (768), Expect = 2e-80

Identities = 149/277 (53%), Positives = 205/277 (73%), Gaps = 3/277 (1%)

```
Query: 14  VQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVERE- 72
          +Q+TQKIT+AM+MV+TSKMRKTQ+RM A+RPY+E +R V++H+++A+      HP L  RE
Sbjct: 1   MQNTQKITRAMQMVSTSKMRKTQERMRAARPYAEKVRTVMAHLAQANAELGHPLLARRET 60

Query: 73  VKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFN 132
          +K+ GI+++S+D+G+CGGLNVN FK      ++K  ++Q I  D+  +G KG++  +    N
Sbjct: 61  IKRAGIILVSSDKGLCGGLNVNSFKRFFGKVKELQDQGIEVDVCCLGQKGLAAAQRARLN 120

Query: 133  IKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQKPVVQQLVPLP 192
          +      LGD P +E+LIG      +F  Y  GE+DAVYI  Y+  FVNTM  Q+P  ++QL+PL
Sbjct: 121  VVASAVHLGDMPKMEKLIGPLTVLFRQYAEGLDAVYIVYSSFVNTMTKQEPALEQLLPL- 179

Query: 193  ESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVASEQAARMVAMKAA 252
          +      + E  +WDYLYEP+  L++ L+  RYLES +YQA+ +N+ASEQAARMVAMKAA
Sbjct: 180  -TPHHMVVEHSHSWDYLYEPDAPTLMEFLVRRYLESVVYQALAENMASEQAARMVAMKAA 238

Query: 253  TDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          TDNAGN I  LRLVYNKARQA+IT EL+EIVAGAAA+
Sbjct: 239  TDNAGNTIKQLRLVYNKARQAAITTELSEIVAGAAAV 275
```

tr [Q83U82](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 297 bits (760), Expect = 1e-79

Identities = 150/150 (100%), Positives = 150/150 (100%)

```
Query: 22  KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
          KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1   KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82  STDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNKIGQLSGLG 141
          STDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNKIGQLSGLG
Sbjct: 61  STDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNKIGQLSGLG 120

Query: 142  DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
          DTPALEELIGVANTMFDAYRNGEIDAVYIA
Sbjct: 121  DTPALEELIGVANTMFDAYRNGEIDAVYIA 150
```

tr [Q83V88](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 296 bits (759), Expect = 2e-79

Identities = 149/150 (99%), Positives = 150/150 (99%)

```
Query: 22  KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
```

Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60
Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPALEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150

tr Q83V83 **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA**
influenzae]

[align](#)

Score = 296 bits (758), Expect = 2e-79
Identities = 148/150 (98%), Positives = 150/150 (99%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFL+EREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLIEREVKKIGILVI 60
Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPALEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150

tr Q83V86 **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus 150 AA**
influenzae]

[align](#)

Score = 295 bits (756), Expect = 4e-79
Identities = 148/150 (98%), Positives = 150/150 (99%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60
Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120
Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPAL+ELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPALQELIGVANTMFDAYRNGEIDAIYIA 150

tr Q9RQ80 **Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera 290 AA**

aphidicola]align

Score = 295 bits (756), Expect = 4e-79

Identities = 145/289 (50%), Positives = 214/289 (73%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA KEIKT+I SV +T+KITKAMEMVA SKMRKT++RM++ RPYSE IR VI+HV++
 Sbjct: 1 MASIKEIKTQITSVVNTKKITKAMEMVAISKMRKTEERMSSGRPYSEIIRKVINHVAQGH 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + YKH +L R++K+IG++++S+DRG+CG LN NLF+ L +I+N+ ++NI DL L G
 Sbjct: 61 LEYKHSYLETRKIKRIGLIIVSSDRGLCGSLNSNLFKVLFKIQNFTQKNIPCDLILFGL 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K + F+ NI +++ LG+ P + ++I + + Y+ ID ++IAYN+F N MS
 Sbjct: 121 KSLPVFKLCENNILSKITHLGEHPNILKVINIGIDVLLKKYQIKRIDKIFIAYNEFHNMMS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
 Q P + QL+PL K + ++ ++ WDYLYE E K+++DSL RY+ESQ+YQ++++N+AS
 Sbjct: 181 QYPKIIQLLPLSRIKSETISTKR--WDYLYESESCLIIDSLFKRYIESQVYQSILENIAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E AARM+AMK AT+N+ I +L+L+YNK RQA+IT EL EI+AGA+A+
 Sbjct: 239 EHAARMMAMKTATENSTERIKELKLLYNKVRQATITQELTEIIAGASAV 287

tr Q9JW71 **ATP synthase gamma chain (EC 3.6.1.34) [ATPG]** 291 AA
[Neisseria align
meningitidis (serogroup A)]

Score = 295 bits (755), Expect = 5e-79

Identities = 150/291 (51%), Positives = 211/291 (71%), Gaps = 2/291 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA KEI TKI SVQ+TQKITKAM+MV+TSKMRKTQ+RM +RPY+E +R V+SH+++ +
 Sbjct: 1 MAVGKEILT KIRS VQNTQKITKAMQM VSTSKMRKTQERMRLARPYAEKVRMVMSHLAQTN 60

Query: 61 IGYKHPFLVE-REVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
 + P L RE++++G ++I++D+G+CGGLN N+ K L Q++ ++ Q I ++ +G
 Sbjct: 61 TDHGIPLLESHREIRRVGFILITSDKGLCGGLNANVLKKFLAQVQEYQNQGIEEEIVCLG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
 SKG+ +S G N+ LGDTP +E L+G +F Y EID +++ Y+ FVNTM
 Sbjct: 121 SKGLMACQSIGLNVVASAVNLGDTPKMEMLLGPLTELFQRYEKHEIDRIHLVYSGFVNTM 180

Query: 180 SQKPVVQQLVPLPESK-DDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNV 238
 Q+P ++ L+P+ E+ D + +W+Y YEP +L+ L+ RYLES +YQA+ DN+
 Sbjct: 181 RQEPRMEVLLPIGENVIGDSAPKSPFSWEYRYEPTALAVLEYLVRRYLESVYVYQALSDNM 240

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 ASEQAARMVAMKAATDNAGN I +LRLVYNK+RQA+IT EL+EIVAGAAA+
 Sbjct: 241 ASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAATTELSEIVAGAAAV 291

tr Q83U83 **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

align

Score = 295 bits (755), Expect = 5e-79

Identities = 148/150 (98%), Positives = 149/150 (98%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTP LEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPVLEELIGVANTMFDAYRNGEIDAIYIA 150

tr Q9JXQ1 **ATP synthase F1, gamma subunit [NMB1935] [Neisseria meningitidis (serogroup B)]**

291

AA

align

Score = 295 bits (754), Expect = 7e-79

Identities = 150/291 (51%), Positives = 210/291 (71%), Gaps = 2/291 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA KEI TKI SVQ+TQKITKAM+MV+TSKMRKTQ+RM +RPY+E +R V+SH+++ +
Sbjct: 1 MAVGKEILTKIRSVQNTQKITKAMQMVSTSKMRKTQERMRLARPYAEKVRMVMSHLAQTN 60

Query: 61 IGYKHPFLVE-REVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
+ P L RE++++G ++I++D+G+CGGLN N+ K L Q++ ++ Q I ++ G
Sbjct: 61 TDHGIPLLESHREIRRVGFILITSDKGLCGGLNANVLKKFLAQVQEYRNQGIEEEIVCFG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
SKG+ +S G N+ LGDTP +E L+G +F Y EID +++ Y+ FVNTM
Sbjct: 121 SKGLMACQSIGLNVVASAVNLGDTPKMEMLLGLPLTELFRYKHEIDRIHLVYSGFVNTM 180

Query: 180 SQKPVVQQLVPLPESK-DDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNV 238
Q+P ++ L+P+ E+ D + +W+Y YEP +L+ L+ RYLES +YQA+ DN+
Sbjct: 181 RQEPRMEVLLPIGENVIGDSAPKSPFSWEYRYEPTALAVLEYLVRRYLESVVYQALSDNM 240

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
ASEQAARMVAMKAATDNAGN I +LRLVYNK+RQA+IT EL+EIVAGAAA+
Sbjct: 241 ASEQAARMVAMKAATDNAGNAIKELRLVYNKSRQAAITTELSEIVAGAAAV 291

tr Q83V85 **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

align

Score = 294 bits (753), Expect = 9e-79

Identities = 148/150 (98%), Positives = 149/150 (98%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPALEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150

tr [Q83V87](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 294 bits (752), Expect = 1e-78
Identities = 149/150 (99%), Positives = 149/150 (99%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVE EVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVECEVKKIGILVI 60

Query: 82 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPALEELIGVANTMFDAYRNGEIDAVYIA
Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAVYIA 150

tr [Q83UA6](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 293 bits (750), Expect = 2e-78
Identities = 147/150 (98%), Positives = 149/150 (99%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSK+RKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKLRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTPALEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPALEELIGVANTMFDAYRNGEIDAIYIA 150

tr [Q83V84](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 293 bits (750), Expect = 2e-78
Identities = 147/150 (98%), Positives = 149/150 (99%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIR+VISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRSVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
DTP LEELIGVANTMFDAYRNGEIDA+YIA
Sbjct: 121 DTPVLEELIGVANTMFDAYRNGEIDAIYIA 150

tr [Q83V89](#) **ATP synthase F1 epsilon subunit (Fragment) [ATPG] [Haemophilus influenzae]** 150 AA

[align](#)

Score = 292 bits (748), Expect = 4e-78
Identities = 148/150 (98%), Positives = 148/150 (98%)

Query: 22 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 81
KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI
Sbjct: 1 KAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYKHPFLVEREVKKIGILVI 60

Query: 82 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 141
STDRGMC GGLNVNLFKT LNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG
Sbjct: 61 STDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGISFFRSFGFNIKGQLSGLG 120

Query: 142 DTPALEELIGVANTMFDAYRNGEIDAVYIA 171
D PALEELIGVANTMFDAYRNGEIDAVYIA
Sbjct: 121 DMPALEELIGVANTMFDAYRNGEIDAVYIA 150

tr [Q9RQ74](#) **Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera aphidicola]** 289 AA

[align](#)

Score = 268 bits (684), Expect = 9e-71
Identities = 138/289 (47%), Positives = 199/289 (68%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
M+ KE++ KI + +TQKITKAMEMV+ SKM+K + +M + RPY +TI+ +I++ +
Sbjct: 1 MSEIKEVRNKKIKCITNTQKITKAMEMVSISKMKKAEVKMNSGRPYLKTIKEIINNFIINN 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMC GGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
Y+H +L +R VKKIGI++ISTDRG+CG LNV LFK L+ I+N+ +NI++DL ++G
Sbjct: 61 TRYQHVVYLEQRAVKKIGIIIIISTDRGLCGNLNVTFLFKKILDFIQYNNRNITSLSILGL 120

```

Query: 121 KGISFFRSFGFNIKGQLSGLGDTTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          KG+SFF+S   I           +   +   +   Y   GEID +++AYNKF +T+
Sbjct: 121 KGLSFFKSLSNKIVFYFNDYAKNNYTFSDCLNCNSIFMKLYSIGEIDRLFLAYNKFSTLI 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
          Q P + QL+PL + K   ++   WDY+YE + K+LL+ LL   YLE QIYQA ++N S
Sbjct: 181 QIPSIIQLLPLSKKK---IHCHNNHWDYIYESDSKLLLNKLLNNYLEFQIYQASLENYTS 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          EQAARM+AMK ATDN+ +LI +L+++YNKARQ +IT EL EIV+GAAAI
Sbjct: 238 EQAARMIAMKQATDNSKDLIRELQIIYNKARQDNITQELTEIVSGAAAI 286

```

tr Q8D3J4 **AtpG protein [ATPG] [Wigglesworthia glossinidia brevipalpis]** 287 AA

align

Score = 265 bits (676), Expect = 8e-70

Identities = 135/286 (47%), Positives = 199/286 (69%), Gaps = 3/286 (1%)

```

Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M   K+I+ KI   ++ TQ IT AME ++   KM+K+Q+ +   +++PY E I   +++ +   +
Sbjct: 1  MYNIKDIRQKIIGIKKTQSITSAMEKISAIKMKKSQNLNSTKPYYEKISLLLLNKLLFQN 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          I YKHP+L +R++K IG +V+STDRG+ G LN+NLFK L +I   KE+ I+T L LIGS
Sbjct: 61  IKYKHPYLKKRQIKCIGYIVVSTDRGLAGSLNINLFFKLLYEINKSKEKKINTKLVLIGS 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          K ISFFR F   I   +SG+GDTP + ELI           M   Y +   ID +YI NKF+NTM+
Sbjct: 121 KAISFFRFFEDIISTISGIGDTPKISELIKPVQIMLKEYDSNIIDKIYIISNKFINTMT 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
          P +++++P+ K   +   +   +YLYEP+ L +S+L RY+ES IYQ++V+N++S
Sbjct: 181 YVPDIKKVLPISIKS---SIKFKNLNLYLEPDFSSLFESILPRYIESLIYQSIVENISS 237

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA 286
          EQ+ARMVAMK+A DN+ NLI +L L+YNKARQ++IT EL EI+AG+
Sbjct: 238 EQSARMVAMKSAMDNSKNLIEELSLIYNKARQSNITKELTEIIAGS 283

```

sp Q89B40 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Buchnera aphidicola (subsp. Baizongia pistaciae)]** 291 AA
align

Score = 261 bits (667), Expect = 9e-69

Identities = 132/289 (45%), Positives = 202/289 (69%), Gaps = 1/289 (0%)

```

Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M G +EI++K+ S+ +T+KITKAMEMV+ SK+RK + RM +SRPY I VISHV +
Sbjct: 1  MIGIREIRSKMKSINNTKKITKAMEMVSISKLRKIKKRMCSSRPYFNIINQVISHVITGN 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          + + H + +R VK+IG++++STDRG+CG LN LFK L +   ++I +L +IG+
Sbjct: 61  LEHYHTYFNQRNVKRIGVIIIVSTDRGLCGNLNTLLFFKKVLEVLTEHINEHILNNLFVIGT 120

```

Query: 121 KGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 K ++FF+SF NI LS L + + +L+ + + Y +G+ID +++AYNKF +T+
 Sbjct: 121 KALTFFKSFTNNIVFSLSNLKNDFKIIDLMEMIRISLEMYISGKIDKLFLAYNKFNSTII 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
 Q P + QL+P+ + K E ++TWDY+YE KVLL+ +L RY+E QIYQ++++N+
 Sbjct: 181 QTPTLVQLLPILPKPLGK-KEVKKTWDYIYESNSKVLLNVVLNRYIEFQIYQSILENLVC 239

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQA+RM+AMK ATDN+ +L+ L++ YNK RQ+SIT EL EI++GAAA+
 Sbjct: 240 EQASRMLAMKQATDNSADLLKALQMNYNKVRQSSITQELTEIISGAAAV 288

tr Q9RQ77 **Gamma subunit of membrane-bound ATP synthase [ATPG] [Buchnera aphidicola]** 290 AA

align

Score = 256 bits (654), Expect = 3e-67

Identities = 127/289 (43%), Positives = 197/289 (67%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M+ KEIK KI + +T+KITKAMEMV+ +KM+K++ +M + +PY + I+ +ISH+
 Sbjct: 1 MSEKKEIKNKINCISNTKKITKAMEMVSIAMKKSEIKMKSRKPYLDIIKTIISHILYNH 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 I Y+H +L R+ KKIGI+VISTDRG+CG LN++LFK + I +K +N+ + L ++GS
 Sbjct: 61 IKYRHLVLYNNRKTCKIGIIVISTDRGLCGSLNISLFFKKIIQLINIYKNKNVMSLFLIGS 120

Query: 121 KGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 KG+S+F+S ++I + + + + + Y +ID ++++YN+F NT+
 Sbjct: 121 KGVSYFSSSTYDITYYEKIITKNYTFDFCLNFIHSSLEYNTQKIDKLFLSYNQFKNTLV 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
 PV+ QL+PL SK + WDY+YE +LLD+LL Y+ESQIYQ++++N
 Sbjct: 181 YIPVIMQLLPL--SKKIFKGNKNSHWDYIYESNSGILLDTLLNDYIESQIYQSILENCTC 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 EQA+RM++MK ATDN+ +LI LR++YNKARQ +IT EL EI++GA A+
 Sbjct: 239 EQASRMISMKQATDNSDILIKLRILYNKARQDNITQELTEIISGANAV 287

tr Q831A4 **ATP synthase F1, gamma subunit [ATPG] [Enterococcus faecalis (Streptococcus faecalis)]** 302 AA

align

Score = 218 bits (555), Expect = 8e-56

Identities = 118/301 (39%), Positives = 180/301 (59%), Gaps = 15/301 (4%)

Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHV----- 56
 A EIK +IAS + T +ITKAM+MV+ +K+ K++ + + YS IR+V++H+
 Sbjct: 3 ASLNEIKQRIASTKTSQITKAMQMVSAAKLTSEGASKSFQEYSSKIRSVVTHLVAAQL 62

Query: 57 -----SKASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKE 108
 S S G H L +R VKK G +VI++D+G+ GG N ++ K T++ I+ +

Sbjct: 63 SELRETEQSSLSEGNVHMLAQRPVKKTGYIVITSDKGLVGGYNSSILKQTMSMIQEDHD 122

Query: 109 QNISTDLGLIGSKGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAV 168
 N L IG G FF++ G ++ +L GL D P EE+ + T Y+N D +

Sbjct: 123 SNKEYALIAIGGTGADFFKARGIDVSYELRGLTDQPTFEEVRKIVTTATTMYQNEVFDEL 182

Query: 169 YIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTWLDYLYEPEPKVLLDSLLVRYLES 228
 Y+ YN VN+++ + V++++P+ + +Q +YL EP P+ +LD LL +Y ES

Sbjct: 183 YVCYNHHVNSLTSQFRVEKMLPITDLPSEATSSEQ--EYLLEPSPEAILDQLLPQYAES 240

Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAA 288
 IY A++D +E AA M AMK ATDNA N+I+DL + YN+ARQ +IT E+ EIVAGAAA

Sbjct: 241 LIYGAIIDAKTAEHAAGMTAMKTATDNAQNIISDLTISYNRRARQGAIQTQEITEIVAGAAA 300

Query: 289 I 289
 +

Sbjct: 301 L 301

sp P20602 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 285
 ATPG_BACME megaterium] AA
align

Score = 216 bits (549), Expect = 4e-55
 Identities = 117/289 (40%), Positives = 175/289 (60%), Gaps = 5/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA ++I+T+I S + T +ITKAMEMV+ +K+ + + + PY E I+ V+S V+ S

Sbjct: 1 MASLRDIQTRITSTKKTSQITKAMEMVSAAKLNRAEQNAKSFVPYMEKIQEVVSSVALGS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 G HP L R VKK G +VI++DRG+ G N N+ + I+ + + IG

Sbjct: 61 RGASHPMLTARSVKKTGYIVITSDRGLAGAYNSNILRKVSQAIEERHQSPDEYGVIAIGR 120

Query: 121 KGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 G FF G + +++GL D PA ++ G+A+ + +G D +Y+ YN F+NT+S

Sbjct: 121 VGRDFFVKRGIPVLLLEITGLADQPAFADIQGIASQTVQMFADGTFDELYLYYNHFINTIS 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWLDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 Q+ ++L+PL + L + Y +EP + +L+ LL +Y ES IY ++D AS

Sbjct: 181 QEVTEKKLLPLTD-----LQPSGKLVGYEFEPSQEEILEVLLPQYAESLIYGGLLDGKAS 235

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E AARM AMK+ATDNA +LIN+L L YN+ARQA+IT E+ EIV GAAA+

Sbjct: 236 EHAARMTAMKSATDNAKDLINNLTLNRRARQAAITQEITEIVGGAAAL 284

trnew AAQ10089 ATP synthase subunit gamma [ATPG] [Bacillus sp. TA2.A1] 286 AA
align

Score = 211 bits (536), Expect = 1e-53
 Identities = 114/289 (39%), Positives = 182/289 (62%), Gaps = 4/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60

M G +EIK +I SV++T++ITKAM+MVA +K+R+ Q+ +RPY++ I+ VIS ++ +
 Sbjct: 1 MQGMREIKRRIRSVKNTRQITKAMKMVAAKLRRQAETAENARPYADKIKEVISSIAAGT 60
 Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 + HP L R VKK G +VI++DRG+ G N N+ + I+ + +G
 Sbjct: 61 KDFSHPMLEARPVKKTGYMVITS DRGLAGPYNANILRLVSKTIEERHQSKDEYVIFAVGR 120
 Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 KG FF+ G+ + +++G+ DTP+L E+ +A + + + D + I YN+FV+ +
 Sbjct: 121 KGRDFFKKRGYPVVEEVTGISDTPSLTEIQDIAQSAIGMFADETFDKLTIFYNEFVSPIV 180
 Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
 Q+PV +QL+PL + ++ L+ Y YEP+ + +L+ LL +Y E+ IY A++D AS
 Sbjct: 181 QRPVEKQLLPL--TSEEVLDGPVSA--YEYEPDSESVLEVLLPKYAETLIYSALLDAKAS 236
 Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E ARM AM ATDNA ++ L L +N+ARQA+IT E+ EIVAGA A+
 Sbjct: 237 EFGARMTAMGNATDNATEMLETTLTQFNRRARQAAITQEIAEIVAGANAL 285

tr Q8E5U9 **H+-transporting ATP synthase gamma chain [ATPG] [Streptococcus agalactiae (serotype III)]** 293 AA

align

Score = 210 bits (535), Expect = 2e-53

Identities = 113/292 (38%), Positives = 181/292 (61%), Gaps = 3/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
 MAG+ EIK KI S + T KIT AM+MV+++K+ K++ + Y+ IR + +++ K+
 Sbjct: 1 MAGSLSEIKDKILSTEKTSKITSAMQMVS SAKLVKSEQAARDFQVYASKIRQITTNLLKS 60
 Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 + G +P L R VKK G +VI++D+G+ GG N + K ++ I ++ +N +
 Sbjct: 61 DLVSGSDNPMLASRPVKKTGYIVITS DKGLVGGYNSKILKAMMDTITDYHTENDDYAIIS 120
 Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
 IGS G FF++ G N+ +L GL D P+ +++ + + Y+N D +Y+ YN VN
 Sbjct: 121 IGSVGSDFFKARGMNVSFELRGLEDQPSFDQVGKIIAQAVEMYKNELFDELYVCYNHHVN 180
 Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
 +++ + +QQ++P+ E D +E + + EP +V+L+ LL +Y ES IY A++D
 Sbjct: 181 SLTSQVRMQMLPIKELDADEASEDRVITGFELEPNREVILEQLLPQYTESLIYGAIIDA 240
 Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
 Sbjct: 241 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRRARQAAITQEITEIVAGANAL 292

sp Q9K6H4 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus** 285
 ATPG_BACHD **halodurans]** AA

align

Score = 209 bits (532), Expect = 4e-53

Identities = 113/289 (39%), Positives = 176/289 (60%), Gaps = 5/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA ++IK +I S + T++ITKAMEMV+ +K+ ++Q++ + PY++ IR V++ ++ +
Sbjct: 1 MASLRDIKQRINSTKKTKQITKAMEMVSAAKLNRSQEKAQSFLPYTDKIREVVASIAASD 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
HP L ER VKK G +VI++DRG+ G N NL + L I + + IG
Sbjct: 61 TDVSHPMLEERPVKKTGYIVITSDRGLAGAYNSNLIRGLLYTINKRHKSKDEYGIFAIGR 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
G + I +++GL D P ++ +A D + + D +YI YN FV+ +
Sbjct: 121 TGRDLLKKRQLPIISEMTGLSDQPTFNDIKDIAKQTVDMFADEVFDELYIWINHVFVSPK 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
Q ++++PL + L++ + + Y YEP +V+L++LL +Y ES +Y A++D AS
Sbjct: 181 QDVTEKKVLPLTD-----LSDTKVSTTYEYEPNEQVILEALLPQYAESLVYGALLDAKAS 235

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E AARM AM AATDNA NLI++L L YN+ARQA+IT E+ EIV GAAA+
Sbjct: 236 EFAARMTAMSAATDNATNLIDELTSLYNRARQAAITQEITEIVGGAAAL 284

tr Q8E073 **ATP synthase F1, gamma subunit [ATPG] [Streptococcus** 293
agalactiae AA
(serotype V)] align

Score = 208 bits (529), Expect = 9e-53

Identities = 112/292 (38%), Positives = 181/292 (61%), Gaps = 3/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
MAG+ EIK KI S + T KIT AM+MV+++K+ K++ + Y+ IR + +++ K+
Sbjct: 1 MAGSLSEIKDKILSTEKTSKITSAMQMVSAAKLKSEQAARDFQVYASKIRQITTNLLKS 60

Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
+ G +P L R VKK G +VI++D+G+ GG N + K ++ I ++ +N +
Sbjct: 61 DLVSGSDNPMLSSRPVKKTGYIVITSDKGLVGGYNSKILKAMMDTITDYHTENDDYAIIS 120

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
IGS G FF++ G N+ +L GL D P+ +++ + + Y+N D +Y+ YN VN
Sbjct: 121 IGSVGSDFFKARGMNVSFELRGLEDQPSFDQVGKIIAQAVEMYKNELFDELYVCYNHHVN 180

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
+++ + +QQ++P+ E + +E + + EP +V+L+ LL +Y ES IY A++D
Sbjct: 181 SLTSQVRMQMLPIKELDAEEASEDRVITGFELEPNREVILEQLLPQYTESLIYGAIIDA 240

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
+E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
Sbjct: 241 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 292

tr Q814W1 **ATP synthase gamma chain (EC 3.6.3.14) [BC5307] [Bacillus** 286
cereus AA
(strain ATCC 14579 / DSM 31)] align

Score = 207 bits (528), Expect = 1e-52

Identities = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%)

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Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
        MA  ++IK KI S + T +ITKAMEMV+ SK+ + +      + PY E I+ V++ +++ S
Sbjct: 1  MASLRDIKAKINSTKKTSQITKAMEMVSASKLNRAEQNAKSFPYMEKIQEVVASIAQGS 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNIST-DLGLIG 119
        G  HP L  R VK+ G +VI++DRG+ GG N N+ +T  N I+      + +      + ++G
Sbjct: 61  KGINHPMLNARPVKRTGYIVITSDRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG 120

Query: 120  SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
        G  + +  GFNI  ++ GL D P+  ++  +A+      + +G  D +YI YN +V+ +
Sbjct: 121  RLGRDYLKRRGFNIIDEVVGLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHVYSKI 180

Query: 180  SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVA 239
        SQ+      +++PL +  D      + T  Y +EP  + +L  LL +Y ES +Y A++D  A
Sbjct: 181  SQEVTENKILPLTDVASD-----KPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA 235

Query: 240  SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
        SE AARM AMK+ATDNA  +I+ L L +N+ARQA+IT E+ EIV GAAA+
Sbjct: 236  SEHAARMTAMKSATDNAMEVIDSLTSLSFNRARQAAITQEITEIVVGAAAL 285

```

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tr Q81JZ4  ATP synthase F1, gamma subunit [ATPG] [Bacillus anthracis      286
          (strain                                     AA
          Ames)]                                     align

```

Score = 207 bits (528), Expect = 1e-52

Identities = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%)

```

Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
        MA  ++IK KI S + T +ITKAMEMV+ SK+ + +      + PY E I+ V++ +++ S
Sbjct: 1  MASLRDIKAKINSTKKTSQITKAMEMVSASKLNRAEQNAKSFPYMEKIQEVVASIAQGS 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNIST-DLGLIG 119
        G  HP L  R VK+ G +VI++DRG+ GG N N+ +T  N I+      + +      + ++G
Sbjct: 61  KGINHPMLNARPVKRTGYIVITSDRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG 120

Query: 120  SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
        G  + +  GFNI  ++ GL D P+  ++  +A+      + +G  D +YI YN +V+ +
Sbjct: 121  RLGRDYLKRRGFNIIDEVVGLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHVYSKI 180

Query: 180  SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVA 239
        SQ+      +++PL +  D      + T  Y +EP  + +L  LL +Y ES +Y A++D  A
Sbjct: 181  SQEVTENKILPLTDVASD-----KPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA 235

Query: 240  SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
        SE AARM AMK+ATDNA  +I+ L L +N+ARQA+IT E+ EIV GAAA+
Sbjct: 236  SEHAARMTAMKSATDNAMEVIDSLTSLSFNRARQAAITQEITEIVVGAAAL 285

```

```

trnew AAS44331 ATP synthase F1, gamma subunit (EC 3.6.3.14) [ATPG]      286
          [Bacillus                                     AA
          cereus ATCC 10987]                                     align

```

Score = 207 bits (528), Expect = 1e-52

Identities = 113/290 (38%), Positives = 177/290 (60%), Gaps = 6/290 (2%)

```

Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
      MA  ++IK KI S + T +ITKAMEMV+ SK+ + + + PY E I+ V++ +++ S
Sbjct: 1  MASLRDIKAKINSTKKTQSITKAMEMVSASKLNRAEQNAKSFVPYMEKIQEVVASIAQGS 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNIST-DLGLIG 119
      G  HP L  R VK+ G +VI++DRG+ GG N N+ +T  N I+ + + + ++G
Sbjct: 61  KGINHPMLNARPVKRTGYIVITS DRGLAGGYNSNVLRTVSNVIRERHNMDSNQYSIIVLG 120

Query: 120  SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
      G + + GENI ++ GL D P+ ++ +A+ + +G D +YI YN +V+ +
Sbjct: 121  RLGRDYLKRRGFNIIDEVVGSLSDHPSFTDIKDLASRAIAMFADGAYDELYIYYNHVSKI 180

Query: 180  SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVA 239
      SQ+ +++PL + D + T Y +EP + +L LL +Y ES +Y A++D A
Sbjct: 181  SQEVTENKILPLTDVASD-----KPTTAYEFEPSEEEILKVLLPQYAESLVYGALLDGKA 235

Query: 240  SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
      SE AARM AMK+ATDNA +I+ L L +N+ARQA+IT E+ EIV GAAA+
Sbjct: 236  SEHAARMTAMKSATDNAMEVIDSLTSLFNRRARQAAITQEITEIVGGAAAL 285

```

tr Q9RAU1 **H⁺-ATPase cytoplasmic F1-part gamma-subunit (H⁺-ATPase gamma subunit) [ATPG] [Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. lactis) (Streptococcus lactis)]** 289 AA align

Score = 206 bits (525), Expect = 3e-52

Identities = 110/289 (38%), Positives = 176/289 (60%), Gaps = 3/289 (1%)

```

Query: 2  AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISH-VSKAS 60
      A  EIKTKIAS + T +IT AM+MV+ +K++K + A + Y+E +R + + VS +
Sbjct: 3  ASLNEIKTKIASTKKTQSITGAMQMVSAAKLQKAESHAKAFQTYAEKVRKITTDLVSSDN 62

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
      K+P +++REVKK G LVI++DRG+ G N N+ K+ ++ I+ + +G
Sbjct: 63  EPAKNPMMIKREVKKTGylVITS DRGLVGSYNSNLIKSVISNIRKRTNESEYITILALGG 122

Query: 121  KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
      G FF++ + L GL D P EE+ + + Y+ E D +Y+ YN VN++
Sbjct: 123  TGADFFKARNVKVSYVLRGLSDQPTFEEVRAIVTEAVEEYQAEEDLYVCYNHHVNSLV 182

Query: 181  QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSSLVRYLESQIYQAVVDNVA 240
      + +++++P+ S D+ +E+ + EP+ + +L+ LL +Y ES IY ++VD +
Sbjct: 183  SEARMEKMLPI--SFDEKGDEKASLVTFELEPDRETILNQLLPQYAESMIYGSIVDAKTA 240

Query: 241  EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
      E AA M AM+ ATDNA ++INDL + YN+ARQASIT E+ EIVAGA+A+
Sbjct: 241  EHAAGMTAMRTATDNAHSVINDLTIQYNRRARQASITQEITEIVAGASAL 289

```

tr Q8EM82 **H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) [ATPG] [Oceanobacillus iheyensis]** 286 AA align

sp Q9CER9 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Lactococcus 289**
ATPG_LACLA lactis **AA**
(subsp. lactis) (Streptococcus lactis)] **align**

Score = 205 bits (521), Expect = 7e-52

Identities = 110/289 (38%), Positives = 172/289 (59%), Gaps = 3/289 (1%)

Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISH-VSKAS 60
 A EIKTKIAS + T +IT AM+MV+ +K++K + A + Y+E +R + + VS
 Sbjct: 3 ASLNEIKTKIASTKKTSQITGAMQMVSAAKLQKAESHAKAFQIYAEKVRKITTDLVSSDK 62

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 K+P +++REVKK G LVI++DRG+ GG N N+ K+ +N I+ + +G
 Sbjct: 63 EPAKNPMMIKREVKKTGylVITSDRGLVGGYNSILKSVMTIRKRHANESYITILALGG 122

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 G FF++ + L GL D P EE+ + Y+ E D +Y+ YN VN++
 Sbjct: 123 TGADFFKARNVKVSYVLRGLSDQPTFEEVRAIVTEAVTEYQAEEDFELYVCYNHHVNSLV 182

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVAS 240
 +++++P+ + +T++ EP+ + +L+ LL +Y ES IY ++VD +
 Sbjct: 183 SDARMEKMLPISFEESGQQKPSLETfEL--EPDRETILNQLLPQYAESMIYGSIVDAKTA 240

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E AA M AM+ ATDNA ++INDL + YN+ARQASIT E+ EIVAGA+A+
 Sbjct: 241 EHAAGMTAMRTATDNAHSVINDLTIQYNRARQASITQEITEIVAGASAL 289

sp P22482 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 289 AA**
ATPG_BACPF pseudofirmus] **align**

Score = 205 bits (521), Expect = 7e-52

Identities = 112/291 (38%), Positives = 175/291 (59%), Gaps = 5/291 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA ++I+ +I S + T++ITKAM+MV+ +K+ + Q + PY++ IR V++ ++ +
 Sbjct: 1 MASLRDIQGRITSTKKTKQITKAMQMVSAAKLNRAQHNAQSFTPYTDKIREVVAAIASSG 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI-- 118
 HP L ER VKK G +V+++D+G+ GG N +L ++ LN IK + N + G+I
 Sbjct: 61 TEISHPMLEERPVKKTGYIVVTSDKGLAGGYNSLIRSLNTIK--ERHNSPDEYGIIM 118

Query: 119 GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNT 178
 G G F+ G I ++ GL D P ++ +A T + + +G D +Y+ YN FV+
 Sbjct: 119 GRIGRDLFKRGLPIIQEVIGLPDQPEFNDIKNIARTSVEMFADGIFDELYVWYNHFVSP 178

Query: 179 MSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNV 238
 ++Q +L+PL + D + Y YEP + +L+ LL +Y ES IY +++D
 Sbjct: 179 ITQDVTEMKLLPLTDIGSDE-KATSASASYEYEPNEQAILEKLLPQYAESLIYGSLLDAK 237

Query: 239 ASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 ASE ARM AM AATDNA LI +L L +N+ARQA+IT E+ EIV GAAA+
 Sbjct: 238 ASEFGARMTAMSAATDNASALIEELTLKFNRRARQAAITQEITEIVGGAAAL 288

tr Q8CNJ6 **ATP synthase gamma chain [SE1701] [Staphylococcus epidermidis]** 288 AA

align

Score = 205 bits (521), Expect = 7e-52

Identities = 105/289 (36%), Positives = 178/289 (61%), Gaps = 2/289 (0%)

```
Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MA KEI ++I S      ++ITKAM MV++SK+R+ +      + RPY E +++ I+ V+ ++
Sbjct: 1  MASLKEIDSRIKSTSKMKQITKAMNMVSSSKLRRAEKNTKSFRPYMEKMQDAITAVAGSN 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          HP L  R++K+ G LVI++D+G+ G  + N+ K+ +N I +      +      L ++G
Sbjct: 61  STSNHPMLKSRDIKRSGLVITSBKGLAGAYSTNVLKSLVNDINSKHNSSEYSILVVGQ 120

Query: 121  KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          +G+ FF+  G+ I+ L  + D P+ + +  +A  D +      ID + I Y+ +V+ +
Sbjct: 121  QGVDFFKHRGYEIESSSLVEVPDQPSFKSIQSIKHAIDLFSSEENIDELTIYYSHYVSVLE 180

Query: 181  QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
          KP  +Q++PL  S++D      Q  Y +EP+ + +L  +L +Y+ES IY  ++D  AS
Sbjct: 181  NKPATKQVLPL--SQEDSGQGHGQMSSYEFEPDKESILSVILPQYVESLIYGTILDAKAS 238

Query: 241  EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          E A+RM AM+ A+DNA  LI+DL L YN+ARQA+IT ++  EIV G++A+
Sbjct: 239  EHASRMTAMRNASDNATELIDDLSEYNRRARQAAITQQITEIVGGSSAL 287
```

tr O05432 **ATP synthase subunit gamma [ATPG] [Moorella thermoacetica 282 AA
(Clostridium thermoaceticum)]**

align

Score = 204 bits (520), Expect = 1e-51

Identities = 114/289 (39%), Positives = 172/289 (59%), Gaps = 8/289 (2%)

```
Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MA  +++K +I SVQSTQ IT+AM+MVA +K+RK Q ++ A RPY+  + V+  + A
Sbjct: 1  MAHMRDLKRRIRSVQSTQHITRAMKMVAAAKLRKAQAQVTAGRPYAAKLEEVVGRMAAV 60

Query: 61  IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
          P      REVKK G ++I+ DRG+ GG N NL + T  +++  E+      L  +G
Sbjct: 61  DPETQPLAATREVKKAGYVLITADRGLAGGYNANLIRLTEERLR---EEGRPAALVAVGR 117

Query: 121  KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
          KG FFR      I  + +GD P L +  +A +  Y  G +D V +  +F + +
Sbjct: 118  KGRDFFRRRPVEIVKSFTDIGDNPELIQARELARQLVTMYLEGLTLDEVNLINTRFYSP 177

Query: 181  QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
          Q P+V++L+P+  +      E++ T DY+YEP P+ +L  LL RY E ++Y+A+++ AS
Sbjct: 178  QVPMVERLLPIATPR-----EKKDGTGYIYEPSPEGVLRVLLPRYCEIKVYRALLEAKAS 232

Query: 241  EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          E  ARM AM  AT NA  +I+  L  +N+ARQA+ITNE+  EIVAGA A+
Sbjct: 233  EHGARTAMDNATKNAAEMIDKFTLSFNRRARQAAITNEIVEIVAGADAL 281
```

sp P09222 **ATP synthase gamma chain precursor (EC 3.6.3.14) [ATPG]** 286
 ATPG_BACP3 **[Bacillus** AA
PS3 (Thermophilic bacterium PS-3)] align

Score = 202 bits (513), Expect = 6e-51
 Identities = 118/289 (40%), Positives = 173/289 (59%), Gaps = 7/289 (2%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 +A ++IKT+I + + T +ITKAMEMV TSK+ + + R RPY E I+ V+++V+ A+
 Sbjct: 4 LASLRDIKTRINATKKTSQITKAMEMVLTSKLNRAEKREIV-RPYMEKIQEVVANVALAA 62

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 HP LV R VKK G LVI++DRG+ G N N+ + I+ + +IG
 Sbjct: 63 RA-SHPMLVSRPVKKTGYLVITS DRGLAGAYNSNVLRRLVYQTIQKRHASPDEYAIIVIGR 121

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
 G+SFFR + ++ L D P+ ++ +A + +G D +Y+ YN +V+ +
 Sbjct: 122 VGLSFFRKRNPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYYNHYVSAIQ 181

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
 Q+ ++L+PL + L E +Q Y +EP + +LD LL +Y ES IY A++D AS
 Sbjct: 182 QEVTERKLLPLTD-----LAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDAKAS 236

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 E AARM AMK ATDNA LI L L YN+ARQA+IT E+ EIVAGA A+
 Sbjct: 237 EHAARMTAMKNATDNANELIRTLTSLYNRARQAAITQEITEIVAGANAL 285

tr Q9A0I8 **Putative proton-translocating ATPase, gamma subunit (EC** 291
3.6.1.34) AA
[ATPG] [Streptococcus pyogenes, Streptococcus pyogenes align
(serotype M18)]

Score = 201 bits (512), Expect = 8e-51
 Identities = 115/292 (39%), Positives = 177/292 (60%), Gaps = 5/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
 MAG+ EIK KI S + T KIT AM MV+++K+ K++ + Y+ IR + + + K+
 Sbjct: 1 MAGSLSEIKAKIISTEKTSKITSAMRMVSSAKLVKSEQAARDFQIYASKIRQITTDLLKS 60

Query: 60 --SIGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 +IG +P LV R VKK G +VI++D+G+ GG N + K+ ++ I + ++
 Sbjct: 61 ELTIGSDNPMLVSRPVKKTGYIVITS DKGLVGGYNSKILKSVM DMITEYHADG-DYEIIS 119

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
 IGS G FF++ G N+ +L GL D P+ E++ + + D + N D +Y+ YN VN
 Sbjct: 120 IGSVGSDFFKARGMNVAFELRGLADQPSFEQVRQIISQSVDMFVNEIFDELYVCYNHHVN 179

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
 +++ + VQQ++P+ + D E T + EP +LD LL ++ ES IY A++D
 Sbjct: 180 SLTSQVRVQQMLPISDLVADEAAEEGVT-GFELEPNRHDILDQLLPQFTESLIYGAIIDA 238

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
 Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

tr Q52412 **TF1-gamma subunit [thermophilic bacterium PS3]** 282 AA
align

Score = 201 bits (511), Expect = 1e-50

Identities = 118/288 (40%), Positives = 172/288 (58%), Gaps = 7/288 (2%)

Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI 61
A ++IKT+I + + T +ITKAMEMV TSK+ + + R RPY E I+ V+++V+ A+
Sbjct: 1 ASLRDIKTRINATKKTSQITKAMEMVLTSKLNRAEKREIV-RPYMEKIQEVVANVALAAR 59

Query: 62 GYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121
HP LV R VKK G LVI++DRG+ G N N+ + I+ + +IG
Sbjct: 60 A-SHPMLVSRPVKKTGYLVITSDRGLAGAYNSNVLRRLVYQTIQKRHASPDEYAIIVIGRV 118

Query: 122 GISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQ 181
G+SFFR + ++ L D P+ ++ +A + +G D +Y+ YN +V+ + Q
Sbjct: 119 GLSFFRKRNMPPVILDITRLPDQPSFADIKEIARKTVGLFADGTFDELYMYNHYVSAIQQ 178

Query: 182 KPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVASE 241
+ ++L+PL + L E +Q Y +EP + +LD LL +Y ES IY A++D ASE
Sbjct: 179 EVTERKLLPLTD-----LAENKQRTVYEFEPSEQEILDVLLPQYAESLIYGALLDAKASE 233

Query: 242 QAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
AARM AMK ATDNA LI L L YN+ARQA+IT E+ EIVAGA A+
Sbjct: 234 HAARMTAMKNATDNANELIRTLTSLYNRARQAAITQEITEIVAGANAL 281

sp P37810 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus** 290
ATPG_BACSU subtilis] AA
align

Score = 201 bits (510), Expect = 1e-50

Identities = 110/289 (38%), Positives = 175/289 (60%), Gaps = 3/289 (1%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
+A ++IK++I S + T +ITKAM+MV+ +K+ + ++ + PY + I+ V+S+V + S
Sbjct: 4 LASLRDIKSRTSTKKTSTQITKAMQMVSAAKLNRAENNAKSFPVPMCKIQEVVSNVGRVS 63

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
KHP L+ REVKK LVI++DRG+ G N ++ ++ ++ + + IG
Sbjct: 64 GNVKHPMLLSREVKKTAYLVITSDRGLAGAFNSSVLR SAYQAMQERHQS KDEYAVIAIGR 123

Query: 121 KGISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
G FF+ I +L+GLGD E+ +A + +G D +++ YN FV+ ++
Sbjct: 124 VGRDFFKKREIPIISELTGLGDEVTFTEIKDLARQTIQMFDIDGAFDELHLVYNHFVSAIT 183

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
Q+ ++L+PL D ++T Y +EP + +L+ LL +Y ES I+ A++D+ AS
Sbjct: 184 QEVTEKKLLPL---SDLGSGGGKRTASYEFEPSEEEVLEVLLPQYAESLIFGALLDSKAS 240

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E AARM AMK ATDNA LI+ L L YN+ARQA+IT E+ EIV GAAA+
Sbjct: 241 EHAARMTAMKNATDNAKELIDSLSLSYNRARQAAITQEITEIVGGAAAL 289

tr Q99SF4 **ATP synthase gamma chain [ATPG] [Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2)]** 288
AA
align

Score = 201 bits (510), Expect = 1e-50

Identities = 106/289 (36%), Positives = 174/289 (59%), Gaps = 2/289 (0%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA KEI T+I S + ++ITKAM MV++SK+R+ + PY + +++ I+ V+ AS
Sbjct: 1 MASLKEIDTRIKSTKKMKQITKAMNMVSSSKLRRAEKNTKQFTPYMDKMQDAITAVAGAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
HP L R++ + G LVI++D+G+ G + N+ K + I+ + + + ++G
Sbjct: 61 SNTNHPMLRPRKITRSGYLVITSDKGLAGAYSANVLKKLITDIEAKHQDSSEYSIVVLGQ 120

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
+G+ F ++ G++I+ + D P+ + + +AN D Y EID + I Y+ +V+ +
Sbjct: 121 QGVDFLKNRGYDIEYSQVDVPDQPSFKSVQALANHAIDLSEEEIDELNIYYSHYVSVLE 180

Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVAS 240
KP +Q++PL S++D Y +EP+ + +L +L +Y+ES IY ++D AS
Sbjct: 181 NKPTSQRVLPL--SQEDSSKGHGLSSYEFEPDKESILSVILPQYVESLIYGTILDAKAS 238

Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E A RM AMK ATDNA LI+DL L YN+ARQA IT ++ EIV G+AA+
Sbjct: 239 EHATRMATAMKNATDNATELIDDLSEYNNRARAETQQITEIVGGSAAAL 287

tr O50158 **Proton-translocating ATPase, gamma subunit [ATPG] [Streptococcus bovis]** 291
AA
align

Score = 201 bits (510), Expect = 1e-50

Identities = 115/292 (39%), Positives = 178/292 (60%), Gaps = 5/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
MAG+ EIK KI S Q T IT AM+MV+ +K+ K++ + Y+ IR + + + K+
Sbjct: 1 MAGSLSEIKGKIISTQKTSHITGAMQMVSAAKLTQSEQAAKDFQVYASKIRQITDLLKS 60

Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
+ G K+P L R VKK G +VI++D+G+ GG N + K ++ I+ + Q+ + +
Sbjct: 61 ELVNGSKNPMLAARPVKKTGYIVITSDKGLVGGYNSKILKAMMDLIEEY-HQDGNYAIIA 119

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
IG G FF++ G N+ +L GL D P+ E++ + + Y+N D +Y+ YN VN
Sbjct: 120 IGGIGADFFKARGMNVVFEELRGLEDQPSFEQVGNIIAKSVEMYKNELFDELYVCYNHHVN 179

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
+++ + VQQ++P+ E D E + + EP +++L+ LL +Y ES IY A+VD
Sbjct: 180 SLTSQVRVQQLPIAELDADEAAEEGVS-GFELEPNREMILEQLLPQYTESLIYGAIYDA 238

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289

+E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
 Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

tr Q8K827 Putative proton-translocating ATPase gamma subunit 291
 [SPYM3_0498] AA
 [Streptococcus pyogenes (serotype M3)] align

Score = 200 bits (509), Expect = 2e-50

Identities = 114/292 (39%), Positives = 177/292 (60%), Gaps = 5/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
 MAG+ EIK KI S + T KIT AM MV+++K+ +++ + Y+ IR + + + K+
 Sbjct: 1 MAGSLSEIKAKIISTEKTSTKITSAMRMVSSAKLVRSEQAARDFQIYASKIRQITDILLKS 60

Query: 60 --SIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 +IG +P LV R VKK G +VI++D+G+ GG N + K+ ++ I + ++
 Sbjct: 61 ELTIGSDNPMLVSRPVKKTGYIVITS DKGLVGGYNSKILKSVM DITEYHADG-DYEIIS 119

Query: 118 IGSKGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
 IGS G FF++ G N+ +L GL D P+ E++ + + D + N D +Y+ YN VN
 Sbjct: 120 IGSVGSDFFKARGMNVAFELRGLADQPSFEQVRQIISQSVDMFVNEIFDELYVCYNHHVN 179

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
 +++ + VQQ++P+ + D E T + EP +LD LL ++ ES IY A++D
 Sbjct: 180 SLTSQVRVQQLPISDLVADEAAEEGVT-GFELEPNRHDILDQLLPQFTESLIYGAIIDA 238

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +E AA M AM+ ATDNA N+INDL + YN+ARQA+IT E+ EIVAGA A+
 Sbjct: 239 KTAEHAAGMTAMQTATDNAKNVINDLTIQYNRARQAAITQEITEIVAGANAL 290

tr Q84XB4 Chloroplast ATPase gamma subunit precursor [ATPC] 369
 [Phaeodactylum
 tricornutum] align

Score = 200 bits (508), Expect = 2e-50

Identities = 114/312 (36%), Positives = 187/312 (59%), Gaps = 27/312 (8%)

Query: 4 AKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGY 63
 A I+ +I SV++T+KIT AM++VA +K+R+ QD + A+RP+SET+++V + + G
 Sbjct: 58 ANAIRDRTSVKNTRKITMAMKLVA AAKVRR AQDAVLATRPFSETLQSVFGGLIQR LGGE 117

Query: 64 KH--PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121
 P L EREVKK+ +LVI+ DRG+CGG N + K + K K+ + DL L+G K
 Sbjct: 118 SVDLPLLTEREVKKVTLVITGDRGLCGGYNSFMIKKAEARFKELKKNNGVEADLILVGKK 177

Query: 122 GISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQ 181
 GI++F G+ I+ + G P ++ + +A + + +GE DAV + Y K FV+ ++
 Sbjct: 178 GIAYFERRGYPIRKKYE-TGQNPTAKQALAI AEEVSSTFLSGESDAVELLYTKFVSLIAS 236

Query: 182 KPVVQQLVPLPES----KDDHLNE-----RQQTWDYLYEPEPKVL 217
 P ++ LVP S K D + + ++ D ++E +P +
 Sbjct: 237 SPSIRTLVPFASDITAKGDEVFQLTSESGQFGVERTELDVAAPQEFPNDMIFEQDPIQI 296

Query: 218 LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITN 277
++++L YL QI + + ++VASE AARM +M++A+DNAG+L L L YN+ARQA++T
Sbjct: 297 VNAILPLYLNGQILRTLQESVASELAARMQSMQASD NAGSLAKQLNLEYNRARQAAVTQ 356

Query: 278 ELNEIVAGAAAI 289
EL EI++GA+A+
Sbjct: 357 ELLEIISGASAL 368

sp P12408 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Anabaena** 315
ATPG_ANASP sp. (strain AA
PCC 7120)] align

Score = 198 bits (503), Expect = 9e-50

Identities = 114/315 (36%), Positives = 185/315 (58%), Gaps = 27/315 (8%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
M K I+ +I SV++T+KIT+AM +VA +++R+ Q+++ A+RP+++ + V+ + +
Sbjct: 1 MPNLKSIRDRIQSVKNTKKITEAMRLVAAARVRRRAQEQVIATRPFADRLAQVLYGL-QTR 59

Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
+ ++ P L +REVK +G+LVIS DRG+CGG N N+ + N+ K K + + +
Sbjct: 60 LRFEDVDLPLLKKREVKSVGLLVISGDRGLCGGYNTNVIRRAENRAKELKAEGLDYTFVI 119

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
+G K +FR I +GL P +E +A+ + + + ++D + + Y +FV+
Sbjct: 120 VGRKAEQYFRRREQPIDASYTGLEQIPTADEANKIADELLSLFLSEKVDRIELVYTRFVS 179

Query: 178 TMSQKPVVQQLVPLP----ESKDDHL-----NERQQTW-----DYLYEPEP 214
+S +PV+Q L+PL E+ DD + ERQ D ++E +P
Sbjct: 180 LVSSRPVIQTLLPLDTQGLEAADDEIFRLTTRGGQFQVERQTVTSQARPLPRDMIFEQDP 239

Query: 215 KVLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
+LDSLL YL +Q+ +A+ ++ ASE AARM AM A++NAG LI L L YNKARQA+
Sbjct: 240 VQILDLLPLYLSNQLLRALQESAASELAARMTAMSNASENAGELIKSLSLSYNKARQAA 299

Query: 275 ITNELNEIVAGAAAI 289
IT EL E+V GA A+
Sbjct: 300 ITQELLEVVGGAEAL 314

sp P41010 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus** 287
ATPG_BACCA caldotenax] AA
align

Score = 197 bits (500), Expect = 2e-49

Identities = 118/290 (40%), Positives = 172/290 (58%), Gaps = 8/290 (2%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
+A ++IKT+I + + T +ITKAMEMV+TSK+ + + R RPY E I+ V++ AS
Sbjct: 4 LASLRDIKTRINATKKTSTQITKAMEMVSTSKLNRAEKREIV-RPYMEKIQEVVA--MSAS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTL-NQIKNWKEQNISTDLGLIG 119
HP LV R VKK G LVI++DRG+ G N N+ + + KN + +IG
Sbjct: 61 AARSHPMLVSRPVKKTGYLVITSRGLAGAYNSNVRLVYPKRSKNAMLPPEIAIIVIG 120

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTM 179
 G+SFFR + ++ L D P+ ++ +A + +G D +Y+ YN +V+ +
 Sbjct: 121 RVGLSFFRKRNPVILDITRLPDQPSFADIKIARKTVGLFADGTFDELYMYNHYVSAI 180

Query: 180 SQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVA 239
 Q+ ++L+PL D L E +Q Y +EP + +LD LL +Y ES IY A++D A
 Sbjct: 181 QQEVTERKLLPLT----DFLAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDAKA 236

Query: 240 SEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 SE AARM AMK ATDNA ++I L L YN+ARQA+IT E+ EIVAG A+
 Sbjct: 237 SEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGRNAL 286

sp P42007 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG] [Bacillus 287 AA**
 ATPG_BACST **stearothermophilus]**

[align](#)

Score = 196 bits (499), Expect = 3e-49

Identities = 121/292 (41%), Positives = 175/292 (59%), Gaps = 12/292 (4%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 +A ++IKT+I + + T +ITKAMEMV+TSK+ + R R Y E I+ V+++V AS
 Sbjct: 4 LASLRDIKTRINATKKTQSITKAMEMVSTSKLNRAAKREIV-RSYMEKIQEVVANV--AS 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTD---LGL 117
 G HP LV R VKK G LVI++DRG+ G N N+ + L K K + D + +
 Sbjct: 61 RGRSHPLVSRPVKKTGYLVITSDRGLAGAYNSNVVR--LVYPKRSKNAMLPPDEYAIIV 118

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
 IG G+SFFR + ++ L D P+ ++ +A + +G D +Y+ YN +V+ +
 Sbjct: 119 IGRVGLSFFRKRNPVILDITRLPDQPSFADIKIARKTVGLFADGTFDELYMYNHYVS 178

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
 + Q+ ++L+PL D L E +Q Y +EP + +LD LL +Y ES IY A++D
 Sbjct: 179 AIQQEVTERKLLPLT----DFLAENKQRTVYEFEPSQEEILDVLLPQYAESLIYGALLDA 234

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 ASE AARM AMK ATDNA ++I L L YN+ARQA+IT E+ EIVAG A+
 Sbjct: 235 KASEHAARMTAMKNATDNANDVIRTLTSLYNRARQAAITQEITEIVAGRNAL 286

tr Q927W3 **AtpG protein [ATPG] [Listeria monocytogenes, Listeria innocua] 290 AA**

[align](#)

Score = 195 bits (496), Expect = 6e-49

Identities = 103/289 (35%), Positives = 168/289 (57%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA +IK +I S + T +ITKAM+MV+ +K+ + + + PY I++V++HV+
 Sbjct: 1 MASLIDIKQIRITSTRKTSQITKAMQMVSAAKLGRAESNARSYPYVSKIKDVVTHVASTG 60

Query: 61 IGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
 HP LV R V + G +V+++D G+ G N ++ K +I + + +G

Sbjct: 61 NSSDHPMLVSRPVHRTGYIVLTSDTGLAGSYNSSVIKEVFQEINKKHTSSDEYAIITVGR 120
Query: 121 KGISFFRSFGFNKIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
FF++ N+ ++ G+ D P E+ +A+ + +G D V+I YN +N++S
Sbjct: 121 SARDFFKARQMNVLLEVQGITDHPIFAEIKDIASNTVQMFEDGVYDEVFIYNNHHINSIS 180
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
+ +QL+PL E + Y +EP + +L+ LL +Y+ES I+ A++D A+
Sbjct: 181 SELRKEQLLPLTEFHEKGKETDVLDTTYEFEPSEQEILEVLLPQYVESLIFGALLDAKAA 240
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E AARM AM++ATDNA +LI+DL L YN+ARQA+IT E+ EIV GAAA+
Sbjct: 241 EHAARMTAMRSATDNASDLISDLQYNRARQAAITQEITEIVGGAAAL 289

sp P29710 **ATP synthase gamma chain, sodium ion specific (EC** 281
ATPG_PROMO **3.6.3.15) [ATPG]** AA
[Propionigenium modestum] align

Score = 194 bits (492), Expect = 2e-48
Identities = 109/289 (37%), Positives = 182/289 (62%), Gaps = 9/289 (3%)

Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI 61
A KEIK++I+SVQST++ITKAME+V+++K +K Q + S+PYS ++ V+++++
Sbjct: 1 AAGKEIKSRISVQSTRQITKAMEIVSSTKFKKFQALVNQSKPYSGSMDKVLANLAAGIK 60
Query: 62 GYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120
+HP F + EVK+IGI+V+++DRG+CGG N + K I ++ +S IG
Sbjct: 61 NERHPLFDGKTEVKRIGIIVMTSDRGLCGGFNSSTLKEMEKLIVANPDKEVSVIA--IGK 118
Query: 121 KGISFFRSFGFNKIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
KG + + ++K + L ++ ++ + + + D VY+ YN+F++ +S
Sbjct: 119 KGRDYCKKKDRDLKAEBYIQLIPETMFDKAKEISENIVEYFYEDIFDEVYLIYNEFISALS 178
Query: 181 QKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDNVA 240
+ +V++L+P+ E Q Y++EP + +L SLL +YL Q+YQA+++N AS
Sbjct: 179 TELIVKKLLPIERI-----EVQDNTTYIFEPSVEDILSSLLPKYLNLIQLYQAILENTAS 232
Query: 241 EQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
E +AR AMK ATDNA ++I DL L YN+ RQA+IT E++EIV+GA+A+
Sbjct: 233 EHSARKNAMKNATDNAEDMIKDLTLQYNRERQAAITQEISEIVSGASAL 281

sp Q41075 **ATP synthase gamma chain, chloroplast precursor (EC** 370
ATPG_PHATR **3.6.3.14)** AA
[ATPC] [Phaeodactylum tricornutum] align

Score = 194 bits (492), Expect = 2e-48
Identities = 114/313 (36%), Positives = 185/313 (58%), Gaps = 28/313 (8%)

Query: 4 AKEIKTKIASVQSTQKITKAMEMV-ATSKMRKTQDRMAASRPYSETIRNVISHVSKASIG 62
A I+ +I SV++T+KIT AM++V A K+R+ QD + A+RP+SET+++V + + G
Sbjct: 58 ANAIRDRITSVKNTRKITMAMKLVRAAPKVRRAQDAVLATRPFSETLQSVFGGLIQLRGG 117
Query: 63 YKH--PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGS 120

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      P L EREVKK+ +LVI+ DRG+CGG N + K + K+ + DL L+G
Sbjct: 118 ESDVLLPLTEREVKKVTLVITGDRGLCGGYNSFMIKKAEARFNELKKNNGVEADLILVGK 177

Query: 121 KGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMS 180
      KGI++F GF I+ + G P ++ + +A + + +GE DAV + Y Kfv+ ++
Sbjct: 178 KGIAYFERRGFPIRKYE-TGQNPTAKQALAI AEVSSTFLSGESDAVELLYTKFVSLIA 236

Query: 181 QKPVVQQLVPLPES----KDDHLNE-----RQQTWDYLYEPEPKV 216
      P ++ LVP S K D + + ++ D ++E +P
Sbjct: 237 SSPSIRTLVPFSASDITAKGDEVFQLTSESGQFGVERTELDVAAPQEFPNMIFEQDPIQ 296

Query: 217 LLDSLVLRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASIT 276
      +++++L YL QI + + ++VASE AARM +M++A+DNAG+L L L YN+ARQA++T
Sbjct: 297 IVNAILPLYLNGQILRTLQESVASELAARMQSMQSASDNAGSLAKQLNLEYNRARQAAVT 356

Query: 277 NELNEIVAGAAAI 289
      EL EI++GA+A+
Sbjct: 357 QELLEIISGASAL 369

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sp Q06908      ATP synthase gamma chain, chloroplast precursor (EC      370
  ATPG_ODOSI  3.6.3.14)      AA
                [ATPC] [Odontella sinensis (Marine centric diatom)]      align

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Score = 194 bits (492), Expect = 2e-48

Identities = 111/312 (35%), Positives = 184/312 (58%), Gaps = 27/312 (8%)

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Query: 4  AKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIG- 62
      A I+ +I SV++T+KIT AM++VA +K+R+ QD + A+RP+SET+++V + G
Sbjct: 59 ANAIRDRTSVKNTKKITMAMKLVA AAKVRRQAQDAVLATRPFSETLQSVFGGLIARMGGE 118

Query: 63 -YKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSK 121
      P L +REV K+ ++VI+ DRG+CGG N + K + K+Q ++ D+ LIG K
Sbjct: 119 ALDLPLLTQREVSKVTLVVITGDRGLCGGYNSFMIKKAEARFNELKDQGVACDMVLIGKK 178

Query: 122 GISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQ 181
      GI++F+ G+ I+ G P ++ + ++ + + Y +GE DAV + Y Kfv++ ++
Sbjct: 179 GITYFQRRGYPIRKTFE-TGQNPDSKQALAI SEELLNTYLSGESDAVELLYTKFISLIAS 237

Query: 182 KPVVQQLVP-----LPESKDDHLNERQQTW-----DYLYEPEPKVL 217
      P + L+P L S D ER + D ++E +P +
Sbjct: 238 SPSARTLIPFSASEITQQGDEVFQLTSSGGDFEVERTELEVAEPQDFPNMIFEQDPIQI 297

Query: 218 LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITN 277
      ++S+L YL QI + + ++VASE AARM +M++A+DNAG+L L YN+ARQA++T
Sbjct: 298 INSILPLYLNGQILRTLQESVASELAARMQSMQSASDNAGDLAKRLSTEYNRARQAAVTQ 357

Query: 278 ELNEIVAGAAAI 289
      E+ EIV+GA+A+
Sbjct: 358 EILEIVSGASAL 369

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tr Q8FQ21  H+-ATPase gamma subunit (EC 3.6.3.14) [ATPG] [Corynebacterium 326 AA
  efficiens]
                                           align

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tr Q8KRU9 Subunit gamma [ATPG] [*Ilyobacter tartaricus*] 282 AA
align

Score = 194 bits (492), Expect = 2e-48

Identities = 108/292 (36%), Positives = 181/292 (61%), Gaps = 13/292 (4%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MAG KE+K +I SVQST +ITKAME+V+++K ++ + S+PYS+++ V+ +++
Sbjct: 1 MAGGKELKGRIKSVQSTHQITKAMEIVSSTKFKRFSALVNPSPKPYKSMDRVLENIAAGI 60

Query: 61 IGYKHP-FLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLI- 118
KHP F +++VKKIG++V+++DRG+CGG N TL +++ +N ++ +I
Sbjct: 61 KSEKHPLFDGKKDVKKIGVIVMTSDRGLCGGFN----NATLKKMEALIAENPGKEVSIIA 116

Query: 119 -GSKGISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
G K + +++K + L E+ ++ + + D VY+ YN+FV+
Sbjct: 117 TGKKARDYCNKRNYDLKAEYIQLIPETMFEKAKEISENIVEYHLHADIFDEVYMIYNEFVS 176

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237
M + V+++++P+ E Q+ Y++EP + +L SLL +YL QIYQA+++N
Sbjct: 177 AMQTELVMKRVLPIERV-----EAQENTTYIFEPSVEDILSSLLPKYLNQIYQAIEN 230

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
ASE +AR AMK ATDNA +I DL L YN+ RQA++T E++EIV+GA+A+
Sbjct: 231 TASEHSARKNAMKNATDNAEMIADLNLQYNRERQAAVTQEISEIVSGASAL 282

sp P43452 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] 300
ATPG_ENTHR [*Enterococcus hirae*] AA
align

Score = 193 bits (490), Expect = 3e-48

Identities = 108/303 (35%), Positives = 179/303 (58%), Gaps = 21/303 (6%)

Query: 2 AGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVS----- 57
A EIKT+IAS + T +IT+AM+MV+ SK+ K++ + Y+ +R +++H++
Sbjct: 3 ASLNEIKTRIASTKKTSQITRAMQMVSAKSLTKSEASSQKFQIYANKVREIVTHLTATQL 62

Query: 58 -----KASIGYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQ 109
+ I Y + L+ R VKK G +VI+ D G+ GG N ++ K T++ ++ +
Sbjct: 63 NDIASDNPRGDINY-NSMLISRPVKKTYIVITADGGLVGGYNSSILKQTMSSILEEDHKS 121

Query: 110 NISTDLGLIGSKGISFFRSFGFNIKQLSGLGDTPALEE---LIGVANTMFDAYRNGEID 166
+ IG G FF++ G N+ +L L D P+ +E ++G+A TM Y+N D
Sbjct: 122 PDDYVMIAIGGTGADFFKARGINLAYELRNLSQPSFDEVKIVGMATM---YQNEVFD 178

Query: 167 AVYIAYNKVFNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYL 226
+Y+ YN +N+++ + V+++++P+ + + Q +Y++EP + +L LL +Y
Sbjct: 179 ELYVCYNHHINSLTSQFRVEKMLPISDLDP EEATTFDQ--EYIFEPSKEEILAQLLPQYA 236

Query: 227 ESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA 286
ES IY A+VD +E AA M AMK ATDNA +I+DL + YN+ARQ +IT E+ EIVAGA
Sbjct: 237 ESLIYGAIYDAKTAEHAAGMTAMKTATDNAATIIDDLTVSYNRARQGAITQEITEIVAGA 296

Query: 287 AAI 289

+A+
Sbjct: 297 SAL 299

tr Q8KAW9 **ATP synthase F1, gamma subunit [ATPG] [Chlorobium tepidum]** 292 AA

align

Score = 192 bits (488), Expect = 5e-48

Identities = 105/294 (35%), Positives = 181/294 (60%), Gaps = 9/294 (3%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
M K+I+ ++ V+STQ++TKAM+MVA +K+R+ QDR +RPY+ ++ +++ +S
Sbjct: 1 MPTLKDIRIRLKGVKSTQQVTKAMKMVAAKLRRAQDRAIQARPYAGKLKEMPLASLSTKV 60

Query: 61 IGYKHPFLVERE-VKKIGILVISTDRGMCGLNVNLFKTTLNQI-KNWKEQNISTDLGLI 118
+P L RE V ++++++DRG+CGG N N+ K I + + + +I
Sbjct: 61 DTSVNPLLSPREEVNVLVILVTSRGLCGGFNANIIKMAQRLIHEEYAALHAKGGVTMI 120

Query: 119 --GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFV 176
G+KG FFR G+ + G+ + + +A+ Y +GE+D V + YN+F
Sbjct: 121 CAGTKGTEFFRKRGYKLAAAYPGVFQNLSDSAREIADKASKMYLSGEVDRVVLVYNEFK 180

Query: 177 NTMSQKPVVQQLVPL-PESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235
+ ++ +QL+P+ PE D + + +YLYEP P ++D L+ ++L +Q+++ ++
Sbjct: 181 SVLAPNLRTEQLLPITPEGGD----AKTASSEYLYEPSPAAIIDELVPKHLNTQLWRVML 236

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
++ A+EQAARM AM +AT+NA LI L + YN+ARQA+IT EL+EIVAGA A+
Sbjct: 237 ESNAAEQAARMAAMDSATENAKELIRVLNISYNRARQAAITKELSEIVAGADAL 290

tr Q8RKV3 **H+-ATPase cytoplasmic F1-part gamma-subunit [ATPG]
[Streptococcus
thermophilus]**

292

AA

align

Score = 192 bits (488), Expect = 5e-48

Identities = 107/292 (36%), Positives = 175/292 (59%), Gaps = 4/292 (1%)

Query: 1 MAGA-KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKA 59
MAG+ +EIK KIAS++ T IT AM+MV+ SK+ +++ + Y+ IR + + + +
Sbjct: 1 MAGSLREIKAKIASIKQTSHITGAMQMVSASKLTRSEQAAKDFQIYASKIRQITTDLLHS 60

Query: 60 SI--GYKHPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
+ G +P L R V+K G +VI++D+G+ GG N + K L+ IK + +
Sbjct: 61 ELVNGSSNPMLDARPVKSGYIVITSDKGLVGGYNSTILKAVLDMIKRDHDSSEDEYAIIS 120

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
IG G FF++ N+ +L GL D P+ +++ + + Y+N D +Y+ YN +N
Sbjct: 121 IGGTGSDFFKARNMNVAFELRGLEDQPSFDQVGKIISKAVGMYQNELFDELYVCYNHHIN 180

Query: 178 TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVVDN 237
++S++ V++++P+ + D + +E + EP+ +LD LL +Y ES IY A+VD
Sbjct: 181 SLSREVRVEKMLPIADF-DPNESEGHVLTKEFELEPDRDTILDQLLPQYAESLIYGAIVDA 239

Query: 238 VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +E AA M AM+ ATDNA +INDL + YN+ARQA+IT E+ EIV GA+A+
 Sbjct: 240 KTAEHAAGMTAMQTATDNAKKIINDLTIQYNRARQAAITQEITEIVGGASAL 291

sp P08450 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] 316
 ATPG_SYNP6 [Synechococcus sp. AA
 (strain PCC 6301) (Anacystis nidulans)] align

Score = 191 bits (486), Expect = 8e-48
 Identities = 111/315 (35%), Positives = 184/315 (58%), Gaps = 27/315 (8%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA K I+ +I SV++T+KIT+AM +VA +K+R+ Q+++ ++RP+++ + V++ + +
 Sbjct: 1 MANLKAIRDRIKSVRNRTRKITEAMRLVAAAKVRRRAQEQLSTRPFADRLAQVLAGLQQR- 59

Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 + +++ P L REVK + +LV+S DRG+CGG N N+ + + + Q + +
 Sbjct: 60 LQFENVDLPLLQRREVKTVALLVVSGDRGLCGGYNSNVIRRAEQRARELSAQGLDYKFVI 119

Query: 118 IGSKGISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFN 177
 +G K +F+ I+ SGL P +E +A+ + + +G +D V + Y KF++
 Sbjct: 120 VGRKAGQYFQRREQPIEATYSGLEQIPTAQEANDIADELLSLFLSGTVDRVELVYTKFLS 179

Query: 178 TMSQKPVVQQLVPLPE---SKDDHLN-----ERQQTW-----DYLYEPEP 214
 ++ PVVQ L+PL S DD + ER++ D ++E +P
 Sbjct: 180 LVASNPVVQTLLPLDPQGLASSDDEIFRLTTRGGSFTVEREKLSEVAPLPRDMIFEQDP 239

Query: 215 KVLDSL LVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
 +L +LL YL +Q+ +A+ + ASE AARM AM +A+DNA L+ L LVYNKARQA+
 Sbjct: 240 AQILSALLPLYLSNQLLRALQEAAASELAARMTAMNSASDNANALVGQLTLVYNKARQAA 299

Query: 275 ITNELNEIVAGAAAI 289
 IT EL E+VAGA A+
 Sbjct: 300 ITQELLEVVAGAEAL 314

sp Q05384 ATP synthase gamma chain (EC 3.6.3.14) [ATPG] 315
 ATPG_SYNP1 [Synechococcus sp. AA
 (strain PCC 6716)] align

Score = 191 bits (484), Expect = 1e-47
 Identities = 112/315 (35%), Positives = 181/315 (56%), Gaps = 27/315 (8%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M K I+ +I +++ T+KIT+AM +VA +K+R+ Q+++ ASRP+++ + V+ + +
 Sbjct: 1 MPNLKAIRDRIKTIKTRKITEAMRLVAAAKVRRRAQEQLVMASRPFADRLAQVLYGL-QTR 59

Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 + ++ P L +R VK + +LV++ DRG+CGG N N+ + + + + I L +
 Sbjct: 60 LRFEDANLPLLAKRPVKTVALLVVTGDRGLCGGYNTNVIRRAKERTEELEAEGIKYTLVI 119

Query: 118 IGSKGISFFRSFGFNIKQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFN 177
 +G K +F+ + I SGL P+ E +AN + + + +D V + Y KFV+
 Sbjct: 120 VGRKAAQYFQRDYPIDAVYSGLEQIPSASEAGQIANELLSLFLSETVDRVELIYTKFVS 179

Query: 178 TMSQKPVVQQLVPLP----ESKDD-----HLNERQQTW-----DYLYPEPEP 214
 +S KPVVQ L+PL E+ DD HL ++ D ++E +P
 Sbjct: 180 LISSKPVVQTLLPLDPQGLEAADDEIFRLTTRASHLEVNRKVTSNLPALPPDMIFEQDP 239

Query: 215 KVL LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
 +LD+LL YL +Q+ +A+ + ASE AARM AM A+DNA LI L L YNKARQA+
 Sbjct: 240 VQILDALLPLYLSNQLLRALQEAAASELAARMTAMNNASDNAQTLLIGTLTSLYNKARQAA 299

Query: 275 ITNELNEIVAGAAAI 289
 IT E+ E+VAGA A+
 Sbjct: 300 ITQEILEVVAGAEAL 314

tr Q8DLU1 **H+-transporting ATP synthase gamma chain [ATPC] [Synechococcus 315 AA
 elongatus (Thermosynechococcus elongatus)]**

align

Score = 191 bits (484), Expect = 1e-47
 Identities = 111/315 (35%), Positives = 183/315 (57%), Gaps = 27/315 (8%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 MA K I+ +I +++ T+KIT+AM +VA +K+R+ Q+++ ASRP+++ + V+ + +
 Sbjct: 1 MANLKAIRDRIKTIKDKTRKITEAMRLVAAAKVRRRAQEQVMASRPFADRLAQVLYSL-QTR 59

Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 + ++ P L +R VK + +LV++ DRG+CGG N N+ + +++ + + + L +
 Sbjct: 60 LRFEDVDLPLLAKRPVKTVALLVVTGDRGLCGGYNTNVIRRAKERLQELEAEGLYTLVI 119

Query: 118 IGSKGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKVFVN 177
 +G K +F+ + I SGL P+ E +A+ + + + +D V + Y KVF+
 Sbjct: 120 VGRKAAQYFQRRDYPIDAVYSGLEQIPSAEAGQIASSELLSLFLSETVDRVELIYTKFVS 179

Query: 178 TMSQKPVVQQLVPLP----ESKDD-----HLNERQQ-----TWDYLYPEPEP 214
 +S KPVVQ L+PL E+ DD HL ++ D ++E +P
 Sbjct: 180 LISSKPVVQTLLPLDPQGLETAADDEIFRLTTRGSHLEVNRKVTSTLPALPSDMIFEQDP 239

Query: 215 KVL LDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQAS 274
 +LD+LL YL +Q+ +A+ + ASE AARM AM A+DNA LI L L YNKARQA+
 Sbjct: 240 LQILDALLPLYLNNQLLRALQEAAASELAARMTAMNNASDNAQALIGTLTSLYNKARQAA 299

Query: 275 ITNELNEIVAGAAAI 289
 IT E+ E+VAGA A+
 Sbjct: 300 ITQEILEVVAGAEAL 314

sp P17253 **ATP synthase gamma chain (EC 3.6.3.14) [ATPG]** 314
 ATPG_SYNY3 **[Synechocystis sp.]** AA
 (strain PCC 6803)] align

Score = 190 bits (482), Expect = 2e-47
 Identities = 111/314 (35%), Positives = 182/314 (57%), Gaps = 25/314 (7%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSK-- 58
 M K I+ +I SV++T+KIT+AM +VA +K+R+ Q+++ ++RP+++ + V+ ++

Sbjct: 1 MPNLKAIRDRIQSVKNTKKITEAMRLVAAAKVRRRAQEQVLSTRPFADALAQVLYNLQNRL 60

Query: 59 ASIGYKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI 118
 + + P +RE K + +LV++ DRG+CGG NVN K + K K Q I+ L L+

Sbjct: 61 SFAETELPLFEQREPKAVALLVVTGDRGLCGGYNVNAIKRAEQRAKELKNQGIQIAVKLVLV 120

Query: 119 GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNT 178
 GSK +F +++ + L P E +A+++ + + +D V + Y +FV+

Sbjct: 121 GSKAKQYFGRRDYDVAASYANLEQIPNASEAAQIADSLVALFVSETVDRVELIYTRFVSL 180

Query: 179 MSQKPVVQQLVPLP----ESKDDHL-----NERQQT-----WDYLYEPEPK 215
 +S +PVVQ L PL E+ DD + ER++ D ++E +P

Sbjct: 181 ISSQPVVQTLFPLSPQGLEAPDDEIFRLITRGGKFQVEREKVEAPVESFPQDMIFEQDPV 240

Query: 216 VLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASI 275
 +L++LL Y +Q+ +A+ ++ ASE AARM AM A+DNAG LI L L YNKARQA+I

Sbjct: 241 QILEALLPLYNTNQLLRALQESAASELAARMTAMSNASDNAGQLIGTLTTLNARQAII 300

Query: 276 TNELNEIVAGAAAI 289
 T EL E+VAGA ++

Sbjct: 301 TQELLEVVAGANSL 314

tr Q7NDC0 **ATP synthase gamma chain [ATPC] [Gloeobacter violaceus]** 314 AA
align

Score = 190 bits (482), Expect = 2e-47

Identities = 115/315 (36%), Positives = 190/315 (59%), Gaps = 28/315 (8%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M + I+ +I SV++TQKITKAM +VA +++R+ Q+++ A RP+++ + ++ + ++

Sbjct: 1 MPNLRGIRDRIKSVKNTQKITKAMRLVAAARVRRRAQEQVLAGRPFADRLVGLLFRRL-RSR 59

Query: 61 IGYKH---PFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGL 117
 + ++ P + R+V+K+ +LVI+ DRG+CG N N+ + T+ ++ ++Q L L

Sbjct: 60 LRFEDVQSPLMERRDVQKVLVLVIAGDRGLCGAYNSNIIRRTVQYLRELQQQKGQFALYL 119

Query: 118 IGSKGISFFRSFGFNIKGQLSGLGDTPALEELIG-VANTMFDAYRNGEIDAVYIAYNKFV 176
 +G+K ISFFR F I L+ + LE + + + + +GE D V + Y +FV

Sbjct: 120 VGNKAISFFRRSNFPIAKTLTNVDPNPTLEGANQLITDDILAPFLSGEYDQVELVYTRFV 179

Query: 177 NTMSQKPVVQQLVPL-PES---KDDH-----LNERQQTW-----DYLYEPE 213
 + +S +P VQ L+PL P++ ++D L E+QQ D ++E +

Sbjct: 180 SLISSRPTVQTLPLDPDALGQEDETFKLITKGGGFVLREKQQVRTEPEFAADTIFEQD 239

Query: 214 PKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQA 273
 P LLD+LL YL S++ A+ ++ ASE AARM AM AA+DNA L++ L +VYNKARQA

Sbjct: 240 PTQLLDALLPLYLTSEVLHALQESSASELAARMTAMSAASDNAKKLLSTLTIVYNKARQA 299

Query: 274 SITNELNEIVAGAAA 288
 SIT E+ E+V+GA A

Sbjct: 300 SITQEILEVVSGANA 314

sp P50005 **ATP synthase gamma chain, sodium ion specific (EC**

299

ATPG_ACEWO 3.6.3.15)

(Na(+)-translocating ATPase gamma chain) [ATPG]
[Acetobacterium woodii]AA
align

Score = 189 bits (480), Expect = 4e-47

Identities = 111/298 (37%), Positives = 179/298 (59%), Gaps = 21/298 (7%)

Query: 5 KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASIGYK 64
 ++IK +I SV ST +IT AME+VA++K+RK+++ RPY E + I + + S +
 Sbjct: 5 QDIKPRIKSVNSTMQITHAMELVASAKLRKSRELAEGRRPYFEAMIESIGRIVEKSGNAR 64

Query: 65 HPFLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGIS 124
 + F+ +REVKK ++I+ D+G+ GG NVN+ K I + KE + L +GS+G
 Sbjct: 65 NIFMDQREVKKTAYIIITGDKGLAGGYNVNVAKLVEEHITD-KENAV---LFTVGSRRGRD 120

Query: 125 FFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQKPV 184
 FR+ ++I+G+ G+ + P V + + ++NGE D VYIAY Kfv+T++Q
 Sbjct: 121 HFRNREYHIQGEYLGISERPNNFFNAKEVTAIVMEGFKNGEYDEVYIAYTKFVSTITQHAQ 180

Query: 185 VQQLVPLP-----ESKDDH--LNERQQTWDYLYEPEPKVLLDSLLVRYLES 228
 + +L+PL E+K++ +++R+ T YEPEP+ LL L+ + S
 Sbjct: 181 MMKLLPLSREELITSGKVKTTEETKEEKSMSDRELTI-MTYEPEPEELLKYLIPNLVSS 239

Query: 229 QIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGA 286
 +Y +++++ ASEQ AR AM++AT NA +I+ L L YN+ RQA IT E++EIV GA
 Sbjct: 240 TVYGSMIESAASEQGARRTAMESATTNANEMIDGLTLQYNRVRQAPITQEISEIVGGA 297

tr Q7P5L4 ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) 282 AA
 [FNV0981] [Fusobacterium nucleatum subsp. vincentii ATCC
 49256] align

Score = 189 bits (480), Expect = 4e-47

Identities = 105/294 (35%), Positives = 178/294 (59%), Gaps = 17/294 (5%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
 M G KEIK++I SVQST++IT AME+V+T+K ++ + SRPY +++R ++ +++
 Sbjct: 1 MPMGKEIKSRIKSVQSTRQITNAMEIVSTTKFKRYSKLVTESRPYEKSMRKILGNIASGV 60

Query: 61 IGYKHP-FLVEREVKKIGILVISTDRGMCGLNVNLFKTTLNQIKNWKEQNISTDLGLI- 118
 +HP F +EVK I I+VI++DRG+CG N +TL +++ E+N + ++ +I
 Sbjct: 61 KNEEHPLFDGRKEVKISAIIVITSDRGLCGSFN---SSTLKELEKLVEKNRNKNITVIP 116

Query: 119 -GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
 G K I F ++ S + + ++ + + Y N D VY+ YNKF++
 Sbjct: 117 FGRKAIDFISKRNDFSESFSKISPDEMKNKIAGEISEEVVEKYNNHIYDEVYVIYNKFIS 176

Query: 178 TMSQKPVVQQLVPL--PESKDDHLNERQQTWDYLYEPEPKVLLDSLLVRYLESQIYQAVV 235
 + ++++P+ PES+ LN +Y++EP + +L +LL R++ QIYQA++
 Sbjct: 177 ALKYDLTCERIPIARPES---LNS----EYIFEPSAEYILSALLPRFINLQIYQAIL 228

Query: 236 DNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
 +N ASE +AR +M +ATDNA +I L + YN+ RQ++IT E+ EIV GA+A+
 Sbjct: 229 NNTASEHSARKNSMSSATDNADEMIKTLNIKYNRNRQSAITQEITEIVGGASAL 282

Score = 189 bits (479), Expect = 5e-47

Identities = 98/286 (34%), Positives = 174/286 (60%), Gaps = 3/286 (1%)

```

Query: 6   EIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHV--SKASIGY 63
          +IKTKIAS ++T +IT AM+MV+ +K+ ++++      + Y++ +R +++ +      +
Sbjct: 7   DIKTKIASTKNTSQITNAMQMVSAAKLGRSEEAARNFQVYAQKVRKLLTDILHGNGAGAS 66

Query: 64  KHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKGI 123
          +P L+ R VKK G +VI++DRG+ GG N ++ K + + +      ++ IG G
Sbjct: 67  TNPMLISRSVKKTGYIVITSDRGLVGGYNSSILKAVMELKEEYHPDGKGFEMICIGGMGA 126

Query: 124  SFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQKP 183
          FF++ G      +L GL D P+ +++ + + + Y+N D +Y+ YN VNT++ +
Sbjct: 127  DFFKARGIQPLYELRGLSDQPSFDQVRKIISKTVEMYQNELFDELYVCYNHHVNTLTSQM 186

Query: 184  VVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVASEQA 243
          V+Q++P+ + + +E + + + E + +L+ LL ++ ES IY A++D +E A
Sbjct: 187  RVEQMLPIVDLDPNEADE-EYSLTFELETSSREEILEQLLPQFAESMIYGAIIDAKTAENA 245

Query: 244  ARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          A M AM+ ATDNA +INDL + YN+ARQA+IT E+ EIVAGA+A+
Sbjct: 246  AGMTAMQTATDNAKKVINDLTIQYNRARQAAITQEITEIVAGASAL 291

```

tr Q8RGE1 **ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15)** 282 AA
[FN0359] [Fusobacterium nucleatum (subsp. nucleatum)]

[align](#)

Score = 187 bits (476), Expect = 1e-46

Identities = 103/292 (35%), Positives = 174/292 (59%), Gaps = 13/292 (4%)

```

Query: 1   MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          M G KEIK++I SVQST++IT AME+V+T+K ++      + SRPY E++R ++ +++
Sbjct: 1   MPMGKEIKSRIKSVQSTRQITNAMEIVSTTKFKRYSKLVTESRPYEE SMRKILGNIASGV 60

Query: 61  IGYKHP-FLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLI- 118
          HP F +EVK I I+VI++DRG+CG N      +TL +++ E+N + ++ +I
Sbjct: 61  KNEGHPLFDGRKEVKSI AIIIVITSDRGLCGSFN----SSTLKELEKLVEKNKNKNITIIP 116

Query: 119  -GSKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVN 177
          G K I F      + S +      + ++ + + Y N D VY+ YNKF++
Sbjct: 117  FGRKAIDFITKRNYEFSESFSKISPDEMKNKIAGEISEEVVEKYNNHIYDEVYVIYNKFIS 176

Query: 178  TMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDN 237
          +      ++++P+ + + LN      +Y++EP + +L +LL R++ QIYQA+++N
Sbjct: 177  ALRYDLTCERIIPITRPEVE-LNS----EYIFEPSTEYILSALLPRFINLQIYQAILNN 230

Query: 238  VASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
          ASE +AR +M +ATDNA +I L + YN+ RQ++IT E+ EIV GA+A+
Sbjct: 231  TASEHSARKNSMSSATDNADEMIKTLNIIKYNRRNRQSAITQEITEIVGGASAL 282

```

tr Q7MA19 **ATP synthase F1 gamma subunit (EC 3.6.3.14) [ATPG] [Wolinella succinogenes]** 298 AA

align

Score = 187 bits (475), Expect = 2e-46

Identities = 112/296 (37%), Positives = 168/296 (55%), Gaps = 15/296 (5%)

Query: 5 KEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKASI--- 61
KEI+ KI SV++TQK TKAM++V+TSK++K ++ SR Y+E I V + KA I
Sbjct: 6 KEIRKKITSVKNTQKTTKAMKLVSTSKLKAEEMAKRSRVYAERITAVFQEI-KAKIEQN 64

Query: 62 ---GYKHPFLV---EREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDL 115
G + P+ +REVK + I+ ++ D+G+CGG N K + +K QN+ L
Sbjct: 65 GFSGLESPYFTAGEDREVKMVDIVFVTADKGLCGGFNSTTIKEVTRLMAEYKSQNVKVRL 124

Query: 116 GLIGSKGISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKF 175
IG KGISFF + ++S L TP E N + NG D V + +N F
Sbjct: 125 RAIGKKGISFFGFNEVELLDKVSDLSATPDYERAAEFVNKATTDFFINGVTDKVLVHNGF 184

Query: 176 VNTMSQKPVVQQLVPLPESKDDHLNERQQTWDYLYEP--EPKVLLDSLVRYLESQIYQA 233
N +SQ+ VQ L+P+ K D + ++ EP + + +LD L +Y+E +Y A
Sbjct: 185 KNMISQELKVQDLLPI---KADAIEAKESLGMMEVEPSEQEREILDQLAKKYIEFNMYA 241

Query: 234 VVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
++D++A+E +ARM AM AA++NAG L+ L + YNKARQ +IT EL EI G ++
Sbjct: 242 LIDSLAAEHSARMQAMDAASNAGELVKSLTIAYNKARQEAITTELVEINTGVESM 297

tr Q9ZJ02 **Proton-translocating ATPase gamma subunit [Streptococcus sanguis]** 293 AA

293 AA

align

Score = 186 bits (473), Expect = 3e-46

Identities = 102/287 (35%), Positives = 169/287 (58%), Gaps = 4/287 (1%)

Query: 6 EIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVIS---HVSIG 62
+IK KIAS ++T +IT AM+MV+ +K+ K+++ + Y++ +R +++ H +A
Sbjct: 7 DIKNKIASTKNTSQITNAMQMVSAAKLGKSEEAANKFQVYAQVKRKLVTMDMLHGHEAENA 66

Query: 63 YKHPFLVEREVKKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIGSKG 122
H L+ R VKK +VI++DRG+ GG N + K + + ++ IGS G
Sbjct: 67 RHHSMLISRVPVKKSAYIVITS DRGLVGGYNATILKALMELKA EYHPTGEDFEVICIGSVG 126

Query: 123 ISFFRSFGFNIGQLSGLGDTPALEELIGVANTMFDAYRNGEIDAVYIAYNKFVNTMSQK 182
FFR+ G +L GL D P+ +E+ + + + Y+N D +Y+ YN VN+++ +
Sbjct: 127 ADFFRARGIQPVYELRGLADQPSFDEVRKII SKTIEMYQNELFDELYVCYNHHVNSLT SQ 186

Query: 183 PVVQQLVPLPESKDDHLNERQQTWDYLYEPEPKVLLDSLVRYLESQIYQAVVDNVASEQ 242
V+Q++P+ + + +E T + E +LD LL ++ ES IY A++D +E
Sbjct: 187 MRVEQMLPIIDLDPNEADE-DYTLNLELESSRDSILDQLLPQFAESMIYGAIIDAKTAEN 245

Query: 243 AARMVAMKAATDNAGNLINDLRLVYNKARQASITNELNEIVAGAAAI 289
AA M AM+ ATDNA +I+DL + YN+ARQA+IT E+ EIVAGA+A+

Sbjct: 246 AAGMTAMQTATDNAKKVISDLTIQYNRARQAAITQEITEIVAGASAL 292

tr Q9FDR6 **H+-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit)** 325
(EC AA
3.6.1.34) [ATPG] [Corynebacterium glutamicum align
(Brevibacterium flavum)]

Score = 186 bits (472), Expect = 4e-46

Identities = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319 (9%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+ ++ AS
Sbjct: 1 MATIRELRDRIRSVNSTKKITKAQELIATSRITKAQGRVAAAAPYAEIQRVLERLASAS 60

Query: 61 IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
HP L ERE K+ +LV+++DRGM GG N N+ K K E + G
Sbjct: 61 -SLDHPMLREREGGKRAAVLVVTSRGMAGGYNHNVLKAAAELEKLLAESGYEVVRYVTG 119

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFD-----AYRNG----- 163
KG+ +++ ++ G +G P V + D A+R G
Sbjct: 120 KKGVDYYKFRAEDVAGTWTGFSQDPDWAATHNVRRLIDGFTASSEGEAAWREGLNLPEG 179

Query: 164 ----EIDAVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTW-----DYLY 210
D V++ Y +F++ ++Q PVV QL+P+ +D + E+ + DY +
Sbjct: 180 QDIQGFQDVHVYTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 239

Query: 211 EPEPKVLLDSLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 270
EP+ LL++LL +Y+ +++ ++ A+E A+R AMK+ATDNA L+ DL V N+A
Sbjct: 240 EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 299

Query: 271 RQASITNELNEIVAGAAAI 289
RQA IT E+ EIV GA A+
Sbjct: 300 RQAQITQEITEIVGGAGAL 318

tr Q9FAA4 **H+-ATPase gamma subunit [ATPG] [Brevibacterium** 325 AA
flavum] align

Score = 186 bits (472), Expect = 4e-46

Identities = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319 (9%)

Query: 1 MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
MA +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+ ++ AS
Sbjct: 1 MATIRELRDRIRSVNSTKKITKAQELIATSRITKAQGRVAAAAPYAEIQRVLERLASAS 60

Query: 61 IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
HP L ERE K+ +LV+++DRGM GG N N+ K K E + G
Sbjct: 61 -SLDHPMLREREGGKRAAVLVVTSRGMAGGYNHNVLKAAAELEKLLAESGYEVVRYVTG 119

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFD-----AYRNG----- 163
KG+ +++ ++ G +G P V + D A+R G
Sbjct: 120 KKGVDYYKFRAEDVAGAWTGFSDPDWAATHNVRRLIDGFTASSEGEAAWREGLNLPEG 179

Query: 164 ----EIDAVYIAYNKFVNTMSQKPVVQQLVPLPESKDDHLNERQQTW-----DYLY 210

```

          D V++ Y +F++ ++Q PVV QL+P+      +D + E+ +      DY +
Sbjct: 180 QDIQGFQVHVYVTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 239

Query: 211 EPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 270
          EP+  LL++LL +Y+  +++  ++  A+E A+R  AMK+ATDNA  L+ DL  V N+A
Sbjct: 240 EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 299

Query: 271 RQASITNELNEIVAGAAAI 289
          RQA IT E+ EIV GA A+
Sbjct: 300 RQAQITQEITEIVGGAGAL 318

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trnew CAF19915  ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.3.14) [ATPG]          325
               [Corynebacterium
               glutamicum (Brevibacterium flavum)]          AA
                                                           align

```

Score = 186 bits (472), Expect = 4e-46
Identities = 112/319 (35%), Positives = 175/319 (54%), Gaps = 31/319 (9%)

```

Query: 1  MAGAKEIKTKIASVQSTQKITKAMEMVATSKMRKTQDRMAASRPYSETIRNVISHVSKAS 60
          MA  +E++ +I SV ST+KITKA E++ATS++ K Q R+AA+ PY+E I+ V+  ++ AS
Sbjct: 1  MATIRELRDRIRSVNSTKKITKAQELIATSRTKAQGRVAAAAPYAEIQRVLERLASAS 60

Query: 61  IGYKHPFLVEREV-KKIGILVISTDRGMCGGLNVNLFKTTLNQIKNWKEQNISTDLGLIG 119
          HP L ERE  K+  +LV+++DRGM GG N N+ K      K  E      + G
Sbjct: 61  -SLDHPMLREREGGKRAAVLVVTSRGMAGGYNHNVLKKAEELEKLLAESGYEVVRYVTG 119

Query: 120 SKGISFFRSFGFNIKGQLSGLGDTPALEELIGVANTMFD-----AYRNG----- 163
          KG+ +++  ++ G +G  P      V  + D      A+R G
Sbjct: 120 KKGVDYYKFRAEDVAGTWTGFSQDPDWAATHNVRRLIDGFTASSEGEAAWREGLNLPEG 179

Query: 164 ----EIDAVYIAYNKFVNTMSQKPVVQQVLVPLPESKDDHLNERQQTW-----DYLY 210
          D V++ Y +F++ ++Q PVV QL+P+      +D + E+ +      DY +
Sbjct: 180 QDIQGFQVHVYVTEFISMLTQNPVVHQLLPVEPVIEDEIFEKGEDLLSSSGEVEPDYEF 239

Query: 211 EPEPKVLLDSLLVRYLESQIYQAVVDNVASEQAARMVAMKAATDNAGNLINDLRLVYNKA 270
          EP+  LL++LL +Y+  +++  ++  A+E A+R  AMK+ATDNA  L+ DL  V N+A
Sbjct: 240 EPDADTLLEALLPQYVSRRLFSIFLEAAAAESASRRNAMKSATDNATELVKDLSRVANQA 299

Query: 271 RQASITNELNEIVAGAAAI 289
          RQA IT E+ EIV GA A+
Sbjct: 300 RQAQITQEITEIVGGAGAL 318

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Database: EXPASY/UniProt
Posted date: Mar 14, 2004 1:03 PM
Number of letters in database: 451,237,162
Number of sequences in database: 1,414,857

Lambda K H
0.316 0.131 0.358

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 289

length of database: 451,237,162

effective HSP length: 122

effective length of query: 167

effective length of database: 278,624,608

effective search space: 46530309536

effective search space used: 46530309536

T: 11

A: 40

X1: 16 (7.3 bits)


X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.6 bits)

S2: 72 (32.3 bits)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Proteomics tools	Swiss-Prot
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 ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot
Hosted by YPRC Korea Mirror sites: Australia Bolivia Canada China Switzerland Taiwan USA				
Search <input type="text" value="Swiss-Prot/TrEMBL"/> for <input type="text" value="atpg"/>			<input type="button" value="Go"/>	<input type="button" value="Clear"/>

Search in Swiss-Prot and TrEMBL for: atpg

Swiss-Prot Release 42.12 of 15-Mar-2004

TrEMBL Release 25.12 of 15-Mar-2004

- Number of sequences found in Swiss-Prot⁽⁶⁸⁾ and TrEMBL⁽¹³²⁾: **200**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Sequence Retrieval System [SRS](#).

Search in Swiss-Prot: There are matches to 68 out of 146193 entries

ATP6_STRMU (P95784)

ATP synthase gamma chain (EC 3.6.3.14) (ATPase protein 6). {GENE: ATPB OR ATPG OR SMU.1533} - Streptococcus mutans

ATPG_ACEWO (P50005)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) (Na(+)-translocating ATPase gamma chain). {GENE: ATPG OR UNCG} - Acetobacterium woodii

ATPG_ANASP (P12408)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR ALL0004} - Anabaena sp. (strain PCC 7120)

ATPG_BACCA (P41010)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus caldotenax

ATPG_BACHD (Q9K6H4)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BH3755} - Bacillus halodurans

ATPG_BACME (P20602)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus megaterium

ATPG_BACP3 (P09222)

ATP synthase gamma chain precursor (EC 3.6.3.14). {GENE: ATPG} - Bacillus PS3 (Thermophilic bacterium PS-3)

ATPG_BACPF (P22482)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus pseudofirmus

ATPG_BACST (P42007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus stearothermophilus

ATPG_BACSU (P37810)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BSU36820} - Bacillus subtilis

ATPG_BOVIN (P05631)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C} - Bos

taurus (Bovine)

ATPG_BUCAI (P57123)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BU007} - Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrtosiphon pisum symbiotic bacterium)

ATPG_BUCAP (O51873)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BUSG007} - Buchnera aphidicola (subsp. Schizaphis graminum)

ATPG_BUCBP (Q89B40)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BBP007} - Buchnera aphidicola (subsp. Baizongia pistaciae)

ATPG_CHLRE (P12113)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Chlamydomonas reinhardtii

ATPG_DROME (O01666)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATPSYN-GAMMA OR CG7610} - Drosophila melanogaster (Fruit fly)

ATPG_ECOLI (P00837)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG OR PAPC OR B3733 OR C4659 OR Z5231 OR ECS4675 OR SF3813 OR S3955} - Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri

ATPG_ENTHR (P43452)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Enterococcus hirae

ATPG_HAEIN (P43716)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HI0480} - Haemophilus influenzae

ATPG_HELPJ (Q9ZK80)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR JHP1061} - Helicobacter pylori J99 (Campylobacter pylori J99)

ATPG_HELPY (P56082)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HP1133} - Helicobacter pylori (Campylobacter pylori)

ATPG_HUMAN (P36542)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1 OR ATP5C} - Homo sapiens (Human)

ATPG_KLULA (P49377)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR MG15} - Kluyveromyces lactis (Yeast)

ATPG_LACLA (Q9CER9)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR LL1765} - Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

ATPG_METMA (Q60189)

V-type ATP synthase subunit G (EC 3.6.3.14) (V-type ATPase subunit G). {GENE: ATPG OR AHAG OR MM0777.1} - Methanosarcina mazei (Methanosarcina frisia)

ATPG_MOUSE (Q91VR2)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1} - Mus musculus (Mouse)

ATPG_MYCGA (P33257)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MYCGA3050 OR MGA_1174} - Mycoplasma gallisepticum

ATPG_MYCGE (P47640)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MG400} - Mycoplasma

genitalium

ATPG_MYCLE (P45824)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ML1144} - Mycobacterium leprae

ATPG_MYCPN (Q50330)ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MPN599 OR MP243} -
Mycoplasma pneumoniae**ATPG_MYCTU (Q10597)**ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RV1309 OR MT1349 OR
MTCY373.29 OR MB1341} - Mycobacterium tuberculosis, Mycobacterium bovis**ATPG_ODOSI (Q06908)**ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Odontella
sinensis (Marine centric diatom)**ATPG_PASMU (Q9L6B6)**

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR PM1493} - Pasteurella multocida

ATPG_PEA (P28552)ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Pisum
sativum (Garden pea)**ATPG_PHATR (Q41075)**ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} -
Phaeodactylum tricornutum**ATPG_PROMO (P29710)**ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15). {GENE: ATPG OR UNCG} -
Propionigenium modestum**ATPG_RAT (P35435)**ATP synthase gamma chain, mitochondrial (EC 3.6.3.14). {GENE: ATP5C} - Rattus norvegicus
(Rat)**ATPG_RHOBL (P05436)**

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodopseudomonas blastica

ATPG_RHOCA (P72246)ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodobacter capsulatus
(Rhodopseudomonas capsulata)**ATPG_RHORU (P07227)**

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodospirillum rubrum

ATPG_RICPR (O50289)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RP802} - Rickettsia prowazekii

ATPG_SCHPO (O74754)ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR
SPBC1734.13} - Schizosaccharomyces pombe (Fission yeast)**ATPG_SPIOL (P05435)**ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Spinacia
oleracea (Spinach)**ATPG_SPIPL (P50006)**

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Spirulina platensis

ATPG_STRLI (P50007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Streptomyces lividans

ATPG_STRMU (P95788)ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SMU.1529} -
Streptococcus mutans**ATPG_SYNPI (Q05384)**ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp.
(strain PCC 6716)

ATPG_SYN6 (P08450)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPG_SYNY3 (P17253)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SLL1327} - Synechocystis sp. (strain PCC 6803)

ATPG_THIFE (P41169)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Thiobacillus ferrooxidans

ATPG_TOBAC (P29790)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Nicotiana tabacum (Common tobacco)

ATPG_VIBAL (P12990)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNGC} - Vibrio alginolyticus

ATPG_YEAST (P38077)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR YBR039W OR YBR0408} - Saccharomyces cerevisiae (Baker's yeast)

ATPX_ANASP (P12410)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR ALL0008} - Anabaena sp. (strain PCC 7120)

ATPX_ANTSP (Q02852)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Antithamnion sp

ATPX_CYACA (Q9TM29)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanidium caldarium

ATPX_CYAPA (P48085)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Cyanophora paradoxa

ATPX_GALSU (P35012)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Galdieria sulphuraria (Red alga)

ATPX_GUIITH (O78478)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Guillardia theta (Cryptomonas phi)

ATPX_OCHNE (Q40608)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Ochrosphaera neapolitana

ATPX_ODOSI (Q00823)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Odontella sinensis (Marine centric diatom)

ATPX_PORPU (P51245)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Porphyra purpurea

ATPX_RHORU (P15015)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Rhodospirillum rubrum

ATPX_SPIOL (P31853)

ATP synthase B' chain, chloroplast precursor (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Spinacia oleracea (Spinach)

ATPX_SYN1 (Q05367)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6716)

ATPX_SYN6 (P08446)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - Synechococcus sp. (strain PCC 6301) (Anacystis nidulans)

ATPX_SYNY3 (P27183)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR SLL1323} - Synechocystis

sp. (strain PCC 6803)

VATD_SULTO (P22721)

V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D) (Sul-ATPase gamma chain). {GENE: ATPD OR ATPG OR ST1438} - Sulfolobus tokodaii, Sulfolobus acidocaldarius

Search in TrEMBL: There are matches to 132 out of 1070786 entries

O05432

ATP synthase subunit gamma {GENE:ATPG} - Moorella thermoacetica (Clostridium thermoaceticum)

O31083

ATP synthase gamma subunit N-terminus homolog {GENE:ATPG} - Methanosarcina barkeri

O50141

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - Ruminococcus albus

O50158

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - Streptococcus bovis

O66581

ATP synthase F1 gamma subunit {GENE:ATPG2 OR AQ_203} - Aquifex aeolicus

O67829

ATP synthase F1 gamma subunit {GENE:ATPG1 OR AQ_2041} - Aquifex aeolicus

Q42139

H⁺-transporting ATP synthase CHAIN9 - like protein (AT4G32260/F10M6_100) {GENE:ATPG OR F10M6.100 OR AT4G32260} - Arabidopsis thaliana (Mouse-ear cress)

Q7MA19

ATP synthase F1 gamma subunit (EC 3.6.3.14) {GENE:ATPG OR WS0515} - Wolinella succinogenes

Q7NA93

ATP synthase gamma chain {GENE:ATPG OR PLU0041} - Photorhabdus luminescens (subsp. laumondii)

Q7NCS0

ATP synthase b' chain of CF(0) {GENE:ATPG OR GLL2908} - Gloeobacter violaceus

Q7P096

H⁺-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CV0671} - Chromobacterium violaceum

Q7U8W8

Putative ATP synthase subunit B' (EC 3.6.3.14) {GENE:ATPG OR SYNW0491} - Synechococcus sp. (strain WH8102)

Q7UFB6

ATP synthase gamma subunit (EC 3.6.1.34) {GENE:ATPG OR RB10216} - Rhodopirellula baltica

Q7UH04

ATP synthase gamma subunit C-terminus homolog (EC 3.6.1.34) {GENE:ATPG OR RB4917} - Rhodopirellula baltica

Q7V034

ATP synthase B/B' CF(0) (EC 3.6.3.14) {GENE:ATPG OR PMM1454} - Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4)

Q7V5S4

ATP synthase B/B' CF(0) precursor (EC 3.6.3.14) {GENE:ATPG OR PMT1470} - Prochlorococcus marinus (strain MIT 9313)

Q7VA64

ATP synthase gamma chain {GENE:ATPG OR PRO1603} - *Prochlorococcus marinus*

Q7VJ22

~~FoF1~~-type ATP synthase (EC 3.6.3.14) {GENE:ATPG OR HH0428} - *Helicobacter hepaticus*

Q7VPP1

ATP synthase gamma chain {GENE:ATPG OR HD0009} - *Haemophilus ducreyi*

Q7VQV7

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR BFL007} - *Candidatus Blochmannia floridanus*

Q7VU45

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BP3287} - *Bordetella pertussis*

Q7W3A9

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BPP4136} - *Bordetella parapertussis*

Q7WEM8

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BB4606} - *Bordetella bronchiseptica* (*Alcaligenes bronchisepticus*)

Q7XZD7

Hypothetical protein atpG (Fragment) {GENE:ATPG} - *Drosera tokaiensis*

Q7XZD8

Hypothetical protein atpG (Fragment) {GENE:ATPG} - *Drosera tokaiensis*

Q81JZ4

ATP synthase F1, gamma subunit {GENE:ATPG OR BA5548} - *Bacillus anthracis* (strain Ames)

Q82J83

Putative ATP synthase gamma chain {GENE:ATPG OR SAV2882} - *Streptomyces avermitilis*

Q82XP9

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR NE0205} - *Nitrosomonas europaea*

Q831A4

ATP synthase F1, gamma subunit {GENE:ATPG OR EF2609} - *Enterococcus faecalis* (*Streptococcus faecalis*)

Q83AF6

ATP synthase, F1 gamma subunit {GENE:ATPG OR CBU1944} - *Coxiella burnetii*

Q83G90

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR TWT425} - *Tropheryma whipplei* (strain Twist) (*Whipple's bacillus*)

Q83HY1

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR TW343} - *Tropheryma whipplei* (strain TW08/27) (*Whipple's bacillus*)

Q83U82

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83U83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83UA6

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V84

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V85

- Q83V86 ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
- Q83V87 ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
- Q83V88 ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
- Q83V89 ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
- Q84DX7 ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
- Q85FR1 ATP synthase F1 complex gamma chain (Fragment) {GENE:ATPG} - Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii)
- Q87E89 ATP synthase CF0 B' chain (Subunit II) {GENE:ATPG} - Cyanidioschyzon merolae (Red alga) [Chloroplast]
- Q87TT3 ATP synthase gamma chain {GENE:ATPG OR PD0429} - Xylella fastidiosa (strain Temecula1 / ATCC 700964)
- Q88BX3 ATP synthase F1, gamma subunit {GENE:ATPG OR PSPT05600} - Pseudomonas syringae (pv. tomato)
- Q88UU2 ATP synthase F1, gamma subunit {GENE:ATPG OR PP5414} - Pseudomonas putida (strain KT2440)
- Q89X73 H(+)-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR LP_2365} - Lactobacillus plantarum
- Q8D3J4 ATP synthase gamma chain {GENE:ATPG OR BLL0441} - Bradyrhizobium japonicum
- Q8DLP6 AtpG protein {GENE:ATPG OR WIGBR0070} - Wigglesworthia glossinidia brevipalpis
- Q8E073 H+-transporting ATP synthase chain b' {GENE:ATPG OR TLR0432} - Synechococcus elongatus (Thermosynechococcus elongatus)
- Q8E5U9 ATP synthase F1, gamma subunit {GENE:ATPG OR SAG0862} - Streptococcus agalactiae (serotype V)
- Q8E8B9 H+-transporting ATP synthase gamma chain {GENE:ATPG OR GBS0880} - Streptococcus agalactiae (serotype III)
- Q8EM82 ATP synthase F1, gamma subunit {GENE:ATPG OR SO4748} - Shewanella oneidensis
- Q8F2J4 H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR OB2976} - Oceanobacillus iheyensis
- Q8FQ21 ATP synthase F1, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR LA2778} - Leptospira interrogans
- Q8FQ21 H+-ATPase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CE1314} - Corynebacterium efficiens

Q8FYR4ATP synthase F1, gamma subunit {GENE:ATPG OR BR1800} - *Brucella suis*Q8G7B2ATP synthase gamma chain {GENE:ATPG OR BL0358} - *Bifidobacterium longum*Q8KAW9ATP synthase F1, gamma subunit {GENE:ATPG OR CT2032} - *Chlorobium tepidum*Q8KM29F1F0-ATPase subunit gamma {GENE:ATPG} - *Oenococcus oeni* (*Leuconostoc oenos*)Q8KRU9Subunit gamma {GENE:ATPG} - *Ilyobacter tartaricus*Q8PCZ6ATP synthase gamma chain {GENE:ATPG OR XCC0553} - *Xanthomonas campestris* (pv. *campestris*)Q8PGG6ATP synthase gamma chain {GENE:ATPG OR XAC3650} - *Xanthomonas axonopodis* (pv. *citri*)Q8RC16F0F1-type ATP synthase gamma subunit {GENE:ATPG OR TTE0636} - *Thermoanaerobacter tengcongensis*Q8RKV3H⁺-ATPase cytoplasmic F1-part gamma-subunit {GENE:ATPG} - *Streptococcus thermophilus*Q8UC75ATP synthase gamma chain {GENE:ATPG OR ATU2623 OR AGR_C_4756} - *Agrobacterium tumefaciens* (strain C58 / ATCC 33970)Q8VL83ATP synthase F1, subunit gamma (Fragment) {GENE:ATPG} - *Helicobacter pylori* (*Campylobacter pylori*)Q8VV78F0F1-ATPase subunit gamma {GENE:ATPG} - *Colwellia maris* (*Vibrio* sp. (strain ABE-1))Q8XID3ATP synthase gamma subunit {GENE:ATPG OR CPE2188} - *Clostridium perfringens*Q8XU75Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR RSC3318 OR RS02548} - *Ralstonia solanacearum* (*Pseudomonas solanacearum*)Q8Z2Q5ATP synthase gamma subunit {GENE:STY3912 OR ATPG OR T3653} - *Salmonella typhi*Q8Z9S5ATP synthase gamma subunit protein (EC 3.6.1.34) (Membrane-bound ATP synthase, F1 sector, gamma-subunit) {GENE:ATPG OR YPO4122 OR Y4136} - *Yersinia pestis*Q8ZKW8Membrane-bound ATP synthase, F1-sector, gamma-subunit (EC 3.6.3.14) {GENE:ATPG OR STM3866} - *Salmonella typhimurium*Q927W3AtpG protein {GENE:ATPG OR LMO2530 OR LIN2674} - *Listeria monocytogenes*, *Listeria innocua*Q92G87ATP synthase gamma chain {GENE:ATPG OR RC1236} - *Rickettsia conorii*Q92LK7Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR R03035 OR SMC02500} - *Rhizobium meliloti* (*Sinorhizobium meliloti*)Q92VG5Putative ATPGTP-binding protein {GENE:RB0740 OR SMB21236} - *Rhizobium meliloti*

(*Sinorhizobium meliloti*) [Plasmid pSymB (megaplasmid 2)]

Q92VY6

Putative ATPGTP-binding hydroxymethyltransferase protein {GENE:RB0561 OR SMB20821} -
Rhizobium meliloti (*Sinorhizobium meliloti*) [Plasmid pSymB (megaplasmid 2)]

Q93Q45

ATP synthase gamma subunit {GENE:ATPG} - *Clostridium pasteurianum*

Q93U19

ATP synthase gamma-subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U22

ATP synthase gamma-subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U62

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U65

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U68

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U71

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U74

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U77

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U80

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U83

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U86

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U89

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U92

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U95

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U98

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA1

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA4

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA7

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB0

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB3

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB6

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB9

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UC2

- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UC5
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UC8
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD1
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD4
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD7
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UE0
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UE3
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q97PT5
- ATP synthase F1, gamma subunit (Proton-translocating ATPase gamma subunit) (Proton-translocating ATPase, F1 sector, gamma-subunit) (EC 3.6.1.34) {GENE:SP1509 OR ATPG OR SPR1361} - Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6)
Q97ZR2
- ATP synthase subunit G (atpG) (EC 3.6.1.34) {GENE:ATPG OR SSO6175} - Sulfolobus solfataricus
- Q99SF4
- ATP synthase gamma chain {GENE:ATPG OR SAV2104 OR SA1906 OR MW2028} - Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2)
- Q9A0I8
- Putative proton-translocating ATPase, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR SPY0759 OR SPYM18_0817} - Streptococcus pyogenes, Streptococcus pyogenes (serotype M18)
- Q9AHX1
- ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
- Q9FAA4
- H⁺-ATPase gamma subunit {GENE:ATPG} - Brevibacterium flavum
- Q9FDR6
- H⁺-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit) (EC 3.6.1.34) {GENE:ATPG OR CGL1211} - Corynebacterium glutamicum (Brevibacterium flavum)
- Q9HT19
- ATP synthase gamma chain {GENE:ATPG OR PA5555} - Pseudomonas aeruginosa
- Q9JW71
- ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR NMA0518} - Neisseria meningitidis (serogroup A)
- Q9K4D4
- ATP synthase gamma chain {GENE:ATPG OR SCO5372 OR 2SC6G5.16} - Streptomyces coelicolor
- Q9PJ20
- ATP synthase F1 sector gamma subunit (EC 3.6.1.34) {GENE:ATPG OR CJ0106} - Campylobacter jejuni
- Q9PR14
- ATP synthase gamma chain {GENE:ATPG OR UU130} - Ureaplasma parvum (Ureaplasma urealyticum biotype 1)
- Q9RAU1

H⁺-ATPase cytoplasmic F1-part gamma-subunit (H⁺-ATPase gamma subunit) {GENE:ATPG} -
Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. lactis)
(Streptococcus lactis)

[Q9RFL4](#)

ATP synthase subunit gamma {GENE:ATPG} - Salmonella typhimurium

[Q9RGY2](#)

F1F0-ATPase subunit gamma {GENE:ATPG} - Lactobacillus acidophilus

[Q9RQ74](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9RQ77](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9RQ80](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9S5B6](#)

F1F0-ATPase gamma subunit {GENE:ATPG} - Desulfovibrio vulgaris

[Q9SBM3](#)

CFO ATP synthase subunit II {GENE:ATPG} - Volvox carteri f. nagariensis

[Q9Z688](#)

ATP synthase subunit gamma (FOF1-type ATP synthase gamma subunit) {GENE:ATPG OR
CAC2866} - Clostridium acetobutylicum

[Q9ZR72](#)

P-glycoprotein {GENE:ATPGP1 OR T1J8.9} - Arabidopsis thaliana (Mouse-ear cress)

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ATP6_STRMU (P95784)

ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6). {GENE: ATPB OR ATPG OR SMU.1533} - Streptococcus mutans

ATPG_ACEWO (P50005)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15) (Na(+)-translocating ATPase gamma chain). {GENE: ATPG OR UNCG} - Acetobacterium woodii

ATPG_ANASP (P12408)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR ALL0004} - Anabaena sp. (strain PCC 7120)

ATPG_BACCA (P41010)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus caldotenax

ATPG_BACHD (Q9K6H4)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BH3755} - Bacillus halodurans

ATPG_BACME (P20602)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus megaterium

ATPG_BACP3 (P09222)

ATP synthase gamma chain precursor (EC 3.6.3.14). {GENE: ATPG} - Bacillus PS3 (Thermophilic bacterium PS-3)

ATPG_BACPF (P22482)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus pseudofirmus

ATPG_BACST (P42007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Bacillus stearothermophilus

ATPG_BACSU (P37810)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BSU36820} - Bacillus subtilis

ATPG_BOVIN (P05631)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C} - Bos

taurus (Bovine)

ATPG_BUCAI (P57123)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BU007} - Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrtosiphon pisum symbiotic bacterium)

ATPG_BUCAP (O51873)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BUSG007} - Buchnera aphidicola (subsp. Schizaphis graminum)

ATPG_BUCBP (Q89B40)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR BBP007} - Buchnera aphidicola (subsp. Baizongia pistaciae)

ATPG_CHLRE (P12113)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Chlamydomonas reinhardtii

ATPG_DROME (O01666)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATPSYN-GAMMA OR CG7610} - Drosophila melanogaster (Fruit fly)

ATPG_ECOLI (P00837)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG OR PAPC OR B3733 OR C4659 OR Z5231 OR ECS4675 OR SF3813 OR S3955} - Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri

ATPG_ENTHR (P43452)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Enterococcus hirae

ATPG_HAEIN (P43716)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HI0480} - Haemophilus influenzae

ATPG_HELPJ (Q9ZK80)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR JHP1061} - Helicobacter pylori J99 (Campylobacter pylori J99)

ATPG_HELPY (P56082)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR HP1133} - Helicobacter pylori (Campylobacter pylori)

ATPG_HUMAN (P36542)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1 OR ATP5C} - Homo sapiens (Human)

ATPG_KLULA (P49377)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR MGI5} - Kluyveromyces lactis (Yeast)

ATPG_LACLA (Q9CER9)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR LL1765} - Lactococcus lactis (subsp. lactis) (Streptococcus lactis)

ATPG_METMA (Q60189)

V-type ATP synthase subunit G (EC 3.6.3.14) (V-type ATPase subunit G). {GENE: ATPG OR AHAG OR MM0777.1} - Methanosarcina mazei (Methanosarcina frisia)

ATPG_MOUSE (Q91VR2)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP5C1} - Mus musculus (Mouse)

ATPG_MYCGA (P33257)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MYCGA3050 OR MGA_1174} - Mycoplasma gallisepticum

ATPG_MYCGE (P47640)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MG400} - Mycoplasma

genitalium

ATPG_MYCLE (P45824)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ML1144} - Mycobacterium leprae

ATPG_MYCPN (Q50330)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR MPN599 OR MP243} - Mycoplasma pneumoniae

ATPG_MYCTU (Q10597)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RV1309 OR MT1349 OR MTCY373.29 OR MB1341} - Mycobacterium tuberculosis, Mycobacterium bovis

ATPG_ODOSI (Q06908)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Odontella sinensis (Marine centric diatom)

ATPG_PASMU (Q9L6B6)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR PM1493} - Pasteurella multocida

ATPG_PEA (P28552)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Pisum sativum (Garden pea)

ATPG_PHATR (Q41075)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Phaeodactylum tricornutum

ATPG_PROMO (P29710)

ATP synthase gamma chain, sodium ion specific (EC 3.6.3.15). {GENE: ATPG OR UNCG} - Propionigenium modestum

ATPG_RAT (P35435)

ATP synthase gamma chain, mitochondrial (EC 3.6.3.14). {GENE: ATP5C} - Rattus norvegicus (Rat)

ATPG_RHOBL (P05436)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodopseudomonas blastica

ATPG_RHOCA (P72246)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodobacter capsulatus (Rhodopseudomonas capsulata)

ATPG_RHORU (P07227)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Rhodospirillum rubrum

ATPG_RICPR (O50289)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR RP802} - Rickettsia prowazekii

ATPG_SCHPO (O74754)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR SPBC1734.13} - Schizosaccharomyces pombe (Fission yeast)

ATPG_SPIOL (P05435)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - Spinacia oleracea (Spinach)

ATPG_SPIPL (P50006)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Spirulina platensis

ATPG_STRLI (P50007)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - Streptomyces lividans

ATPG_STRMU (P95788)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SMU.1529} - Streptococcus mutans

ATPG_SYNPI (Q05384)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - Synechococcus sp. (strain PCC 6716)

ATPG_SYN6 (P08450)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC} - *Synechococcus* sp. (strain PCC 6301) (*Anacystis nidulans*)

ATPG_SYNY3 (P17253)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR ATPC OR SLL1327} - *Synechocystis* sp. (strain PCC 6803)

ATPG_THIFE (P41169)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG} - *Thiobacillus ferrooxidans*

ATPG_TOBAC (P29790)

ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14). {GENE: ATPC} - *Nicotiana tabacum* (Common tobacco)

ATPG_VIBAL (P12990)

ATP synthase gamma chain (EC 3.6.3.14). {GENE: ATPG OR UNCG} - *Vibrio alginolyticus*

ATPG_YEAST (P38077)

ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). {GENE: ATP3 OR YBR039W OR YBR0408} - *Saccharomyces cerevisiae* (Baker's yeast)

ATPX_ANASP (P12410)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR ALL0008} - *Anabaena* sp. (strain PCC 7120)

ATPX_ANTSP (Q02852)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Antithamnion* sp

ATPX_CYACA (Q9TM29)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Cyanidium caldarium*

ATPX_CYAPA (P48085)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Cyanophora paradoxa*

ATPX_GALSU (P35012)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Galdieria sulphuraria* (Red alga)

ATPX_GUIITH (O78478)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Guillardia theta* (*Cryptomonas phi*)

ATPX_OCHNE (Q40608)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Ochrosphaera neapolitana*

ATPX_ODOSI (Q00823)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Odontella sinensis* (Marine centric diatom)

ATPX_PORPU (P51245)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Porphyra purpurea*

ATPX_RHORU (P15015)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Rhodospirillum rubrum*

ATPX_SPIOL (P31853)

ATP synthase B' chain, chloroplast precursor (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Spinacia oleracea* (Spinach)

ATPX_SYN1 (Q05367)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Synechococcus* sp. (strain PCC 6716)

ATPX_SYN6 (P08446)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG} - *Synechococcus* sp. (strain PCC 6301) (*Anacystis nidulans*)

ATPX_SYNY3 (P27183)

ATP synthase B' chain (EC 3.6.3.14) (Subunit II). {GENE: ATPG OR SLL1323} - *Synechocystis*

sp. (strain PCC 6803)

VATD_SULTO (P22721)

V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D) (Sul-ATPase gamma chain). {GENE: ATPD OR ATPG OR ST1438} - *Sulfolobus tokodaii*, *Sulfolobus acidocaldarius*

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O05432

ATP synthase subunit gamma {GENE:ATPG} - *Moorella thermoacetica* (*Clostridium thermoaceticum*)

O31083

ATP synthase gamma subunit N-terminus homolog {GENE:ATPG} - *Methanosarcina barkeri*

O50141

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - *Ruminococcus albus*

O50158

Proton-translocating ATPase, gamma subunit {GENE:ATPG} - *Streptococcus bovis*

O66581

ATP synthase F1 gamma subunit {GENE:ATPG2 OR AQ_203} - *Aquifex aeolicus*

O67829

ATP synthase F1 gamma subunit {GENE:ATPG1 OR AQ_2041} - *Aquifex aeolicus*

Q42139

H⁺-transporting ATP synthase CHAIN9 - like protein (AT4G32260/F10M6_100) {GENE:ATPG OR F10M6.100 OR AT4G32260} - *Arabidopsis thaliana* (Mouse-ear cress)

Q7MA19

ATP synthase F1 gamma subunit (EC 3.6.3.14) {GENE:ATPG OR WS0515} - *Wolinella succinogenes*

Q7NA93

ATP synthase gamma chain {GENE:ATPG OR PLU0041} - *Photorhabdus luminescens* (subsp. *laumondii*)

Q7NCS0

ATP synthase b' chain of CF(0) {GENE:ATPG OR GLL2908} - *Gloeobacter violaceus*

Q7P096

H⁺-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CV0671} - *Chromobacterium violaceum*

Q7U8W8

Putative ATP synthase subunit B' (EC 3.6.3.14) {GENE:ATPG OR SYNW0491} - *Synechococcus* sp. (strain WH8102)

Q7UFB6

ATP synthase gamma subunit (EC 3.6.1.34) {GENE:ATPG OR RB10216} - *Rhodopirellula baltica*

Q7UH04

ATP synthase gamma subunit C-terminus homolog (EC 3.6.1.34) {GENE:ATPG OR RB4917} - *Rhodopirellula baltica*

Q7V034

ATP synthase B/B' CF(0) (EC 3.6.3.14) {GENE:ATPG OR PMM1454} - *Prochlorococcus marinus* subsp. *pastoris* (strain CCMP 1378 / MED4)

Q7V5S4

ATP synthase B/B' CF(0) precursor (EC 3.6.3.14) {GENE:ATPG OR PMT1470} - *Prochlorococcus marinus* (strain MIT 9313)

Q7VA64

ATP synthase gamma chain {GENE:ATPG OR PRO1603} - *Prochlorococcus marinus*

Q7VJ22

FoF1-type ATP synthase (EC 3.6.3.14) {GENE:ATPG OR HH0428} - *Helicobacter hepaticus*

Q7VPP1

ATP synthase gamma chain {GENE:ATPG OR HD0009} - *Haemophilus ducreyi*

Q7VQV7

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR BFL007} - *Candidatus Blochmannia floridanus*

Q7VU45

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BP3287} - *Bordetella pertussis*

Q7W3A9

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BPP4136} - *Bordetella parapertussis*

Q7WEM8

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR PAPC OR UNCG OR BB4606} - *Bordetella bronchiseptica* (*Alcaligenes bronchisepticus*)

Q7XZD7

Hypothetical protein atpG (Fragment) {GENE:ATPG} - *Drosera tokaiensis*

Q7XZD8

Hypothetical protein atpG (Fragment) {GENE:ATPG} - *Drosera tokaiensis*

Q81JZ4

ATP synthase F1, gamma subunit {GENE:ATPG OR BA5548} - *Bacillus anthracis* (strain Ames)

Q82J83

Putative ATP synthase gamma chain {GENE:ATPG OR SAV2882} - *Streptomyces avermitilis*

Q82XP9

ATP synthase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR NE0205} - *Nitrosomonas europaea*

Q831A4

ATP synthase F1, gamma subunit {GENE:ATPG OR EF2609} - *Enterococcus faecalis* (*Streptococcus faecalis*)

Q83AF6

ATP synthase, F1 gamma subunit {GENE:ATPG OR CBU1944} - *Coxiella burnetii*

Q83G90

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR TWT425} - *Tropheryma whippelii* (strain Twist) (*Whipple's bacillus*)

Q83HY1

ATP synthase gamma chain (EC 3.6.3.14) {GENE:ATPG OR TW343} - *Tropheryma whippelii* (strain TW08/27) (*Whipple's bacillus*)

Q83U82

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83U83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83UA6

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V83

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V84

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - *Haemophilus influenzae*

Q83V85

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
Q83V86

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
Q83V87

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
Q83V88

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
Q83V89

ATP synthase F1 epsilon subunit (Fragment) {GENE:ATPG} - Haemophilus influenzae
Q84DX7

ATP synthase F1 complex gamma chain (Fragment) {GENE:ATPG} - Tropheryma whipplei
(Whipple's bacillus) (Tropheryma whippelii)
Q85FR1

ATP synthase CF0 B' chain (Subunit II) {GENE:ATPG} - Cyanidioschyzon merolae (Red alga)
[Chloroplast]
Q87E89

ATP synthase gamma chain {GENE:ATPG OR PD0429} - Xylella fastidiosa (strain Temecula1 /
ATCC 700964)
Q87TT3

ATP synthase F1, gamma subunit {GENE:ATPG OR PSPTO5600} - Pseudomonas syringae (pv.
tomato)
Q88BX3

ATP synthase F1, gamma subunit {GENE:ATPG OR PP5414} - Pseudomonas putida (strain
KT2440)
Q88UU2

H(+)-transporting two-sector ATPase, gamma subunit (EC 3.6.3.14) {GENE:ATPG OR
LP_2365} - Lactobacillus plantarum
Q89X73

ATP synthase gamma chain {GENE:ATPG OR BLL0441} - Bradyrhizobium japonicum
Q8D3J4

AtpG protein {GENE:ATPG OR WIGBR0070} - Wigglesworthia glossinidia brevipalpis
Q8DLP6

H+-transporting ATP synthase chain b' {GENE:ATPG OR TLR0432} - Synechococcus elongatus
(Thermosynechococcus elongatus)
Q8E073

ATP synthase F1, gamma subunit {GENE:ATPG OR SAG0862} - Streptococcus agalactiae
(serotype V)
Q8E5U9

H+-transporting ATP synthase gamma chain {GENE:ATPG OR GBS0880} - Streptococcus
agalactiae (serotype III)
Q8E8B9

ATP synthase F1, gamma subunit {GENE:ATPG OR SO4748} - Shewanella oneidensis
Q8EM82

H(+)-transporting ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR OB2976} -
Oceanobacillus iheyensis
Q8F2J4

ATP synthase F1, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR LA2778} - Leptospira
interrogans
Q8FQ21

H+-ATPase gamma subunit (EC 3.6.3.14) {GENE:ATPG OR CE1314} - Corynebacterium
efficiens

Q8FYR4

ATP synthase F1, gamma subunit {GENE:ATPG OR BR1800} - *Brucella suis*

Q8G7B2

ATP synthase gamma chain {GENE:ATPG OR BL0358} - *Bifidobacterium longum*

Q8KAW9

ATP synthase F1, gamma subunit {GENE:ATPG OR CT2032} - *Chlorobium tepidum*

Q8KM29

F1F0-ATPase subunit gamma {GENE:ATPG} - *Oenococcus oeni* (*Leuconostoc oenos*)

Q8KRU9

Subunit gamma {GENE:ATPG} - *Ilyobacter tartaricus*

Q8PCZ6

ATP synthase gamma chain {GENE:ATPG OR XCC0553} - *Xanthomonas campestris* (pv. *campestris*)

Q8PGG6

ATP synthase gamma chain {GENE:ATPG OR XAC3650} - *Xanthomonas axonopodis* (pv. *citri*)

Q8RC16

F0F1-type ATP synthase gamma subunit {GENE:ATPG OR TTE0636} - *Thermoanaerobacter tengcongensis*

Q8RKV3

H⁺-ATPase cytoplasmic F1-part gamma-subunit {GENE:ATPG} - *Streptococcus thermophilus*

Q8UC75

ATP synthase gamma chain {GENE:ATPG OR ATU2623 OR AGR_C_4756} - *Agrobacterium tumefaciens* (strain C58 / ATCC 33970)

Q8VL83

ATP synthase F1, subunit gamma (Fragment) {GENE:ATPG} - *Helicobacter pylori* (*Campylobacter pylori*)

Q8VV78

F0F1-ATPase subunit gamma {GENE:ATPG} - *Colwellia maris* (*Vibrio* sp. (strain ABE-1))

Q8XID3

ATP synthase gamma subunit {GENE:ATPG OR CPE2188} - *Clostridium perfringens*

Q8XU75

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR RSC3318 OR RS02548} - *Ralstonia solanacearum* (*Pseudomonas solanacearum*)

Q8Z2Q5

ATP synthase gamma subunit {GENE:STY3912 OR ATPG OR T3653} - *Salmonella typhi*

Q8Z9S5

ATP synthase gamma subunit protein (EC 3.6.1.34) (Membrane-bound ATP synthase, F1 sector, gamma-subunit) {GENE:ATPG OR YPO4122 OR Y4136} - *Yersinia pestis*

Q8ZKW8

Membrane-bound ATP synthase, F1 sector, gamma-subunit (EC 3.6.3.14) {GENE:ATPG OR STM3866} - *Salmonella typhimurium*

Q927W3

AtpG protein {GENE:ATPG OR LMO2530 OR LIN2674} - *Listeria monocytogenes*, *Listeria innocua*

Q92G87

ATP synthase gamma chain {GENE:ATPG OR RC1236} - *Rickettsia conorii*

Q92LK7

Probable ATP synthase gamma chain protein (EC 3.6.1.34) {GENE:ATPG OR R03035 OR SMC02500} - *Rhizobium meliloti* (*Sinorhizobium meliloti*)

Q92VG5

Putative ATPGTP-binding protein {GENE:RB0740 OR SMB21236} - *Rhizobium meliloti*

(*Sinorhizobium meliloti*) [Plasmid pSymB (megaplasmid 2)]

Q92VY6

Putative ATPGTP-binding hydroxymethyltransferase protein {GENE:RB0561 OR SMB20821} -
Rhizobium meliloti (*Sinorhizobium meliloti*) [Plasmid pSymB (megaplasmid 2)]

Q93Q45

ATP synthase gamma subunit {GENE:ATPG} - *Clostridium pasteurianum*

Q93U19

ATP synthase gamma-subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U22

ATP synthase gamma-subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U62

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U65

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U68

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U71

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U74

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U77

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U80

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U83

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U86

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U89

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U92

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U95

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93U98

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA1

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA4

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UA7

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB0

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB3

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB6

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UB9

ATP synthase gamma subunit {GENE:ATPG} - *Carsonella ruddii*

Q93UC2

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UC5

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UC8

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD4

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UD7

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UE0

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q93UE3

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q97PT5

ATP synthase F1, gamma subunit (Proton-translocating ATPase gamma subunit) (Proton-translocating ATPase, F1 sector, gamma-subunit) (EC 3.6.1.34) {GENE:SP1509 OR ATPG OR SPR1361} - Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6)
Q97ZR2

ATP synthase subunit G (atpG) (EC 3.6.1.34) {GENE:ATPG OR SSO6175} - Sulfolobus solfataricus
Q99SF4

ATP synthase gamma chain {GENE:ATPG OR SAV2104 OR SA1906 OR MW2028} - Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2)
Q9A0I8

Putative proton-translocating ATPase, gamma subunit (EC 3.6.1.34) {GENE:ATPG OR SPY0759 OR SPYM18_0817} - Streptococcus pyogenes, Streptococcus pyogenes (serotype M18)
Q9AHX1

ATP synthase gamma subunit {GENE:ATPG} - Carsonella ruddii
Q9FAA4

H⁺-ATPase gamma subunit {GENE:ATPG} - Brevibacterium flavum
Q9FDR6

H⁺-ATPase gamma subunit (F0F1-type ATP synthase gamma subunit) (EC 3.6.1.34) {GENE:ATPG OR CGL1211} - Corynebacterium glutamicum (Brevibacterium flavum)
Q9HT19

ATP synthase gamma chain {GENE:ATPG OR PA5555} - Pseudomonas aeruginosa
Q9JW71

ATP synthase gamma chain (EC 3.6.1.34) {GENE:ATPG OR NMA0518} - Neisseria meningitidis (serogroup A)

Q9K4D4
ATP synthase gamma chain {GENE:ATPG OR SCO5372 OR 2SC6G5.16} - Streptomyces coelicolor

Q9PJ20
ATP synthase F1 sector gamma subunit (EC 3.6.1.34) {GENE:ATPG OR CJ0106} - Campylobacter jejuni

Q9PR14
ATP synthase gamma chain {GENE:ATPG OR UU130} - Ureaplasma parvum (Ureaplasma urealyticum biotype 1)

Q9RAU1

H⁺-ATPase cytoplasmic F1-part gamma-subunit (H⁺-ATPase gamma subunit) {GENE:ATPG} -
Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris), Lactococcus lactis (subsp. lactis)
(Streptococcus lactis)

[Q9RFL4](#)

ATP synthase subunit gamma {GENE:ATPG} - Salmonella typhimurium

[Q9RGY2](#)

F1F0-ATPase subunit gamma {GENE:ATPG} - Lactobacillus acidophilus

[Q9RQ74](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9RQ77](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9RQ80](#)

Gamma subunit of membrane-bound ATP synthase {GENE:ATPG} - Buchnera aphidicola

[Q9S5B6](#)

F1F0-ATPase gamma subunit {GENE:ATPG} - Desulfovibrio vulgaris

[Q9SBM3](#)

CFO ATP synthase subunit II {GENE:ATPG} - Volvox carteri f. nagariensis

[Q9Z688](#)

ATP synthase subunit gamma (FOF1-type ATP synthase gamma subunit) {GENE:ATPG OR
CAC2866} - Clostridium acetobutylicum

[Q9ZR72](#)

P-glycoprotein {GENE:ATPGP1 OR T1J8.9} - Arabidopsis thaliana (Mouse-ear cress)

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L1: Entry 72 of 74

File: DWPI

Aug 11, 2003

DERWENT-ACC-NO: 1998-011056

DERWENT-WEEK: 200408

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TITLE: Bacteria from the family Pasteurellaceae producing repeat in toxin (RTX) - in non-activated form, useful for preparing live attenuated vaccines against Haemophilus, Actinobacillus and Pasteurella.

Basic Abstract Text (1):

Bacteria from the family Pasteurellaceae producing 'repeat in toxin' (RTX) in a nonactivated form are new.

Basic Abstract Text (2):

USE - The bacteria are useful for preparing live attenuated vaccines for protecting animals against infection by an RTX-producing bacterium of the family Pasteurellaceae, especially Actinobacillus pleuropneumoniae or Pasteurella haemolytica (claimed).

Actinobacillus actinomycescomitans
Actinobacillus suis

Actinobacillus pleuropneumoniae ←
Pasteurella anatipestifer
Pasteurella haemolytica ←
Pasteurella multocida ←
Haemophilus parasuis

"

InfluenzaeDucreyiSomnus ←

Pasteurella trehalosi

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L1: Entry 70 of 74

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

Basic Abstract Text (1):

NOVELTY - A gram negative bacteria, such as attenuated Pasteurellaceae, comprising a mutation in a virulence gene, selected from one of 68 defined sequences (N1-N68) (given in the specification), is new.

Basic Abstract Text (4):

(2) a method for producing a gram-negative bacteria mutant, such as attenuated Pasteurellaceae, comprising introducing a mutation into any of N1 to N68, resulting in decreased activity of a gene product encoded by the mutated gene;

Basic Abstract Text (5):

(3) a purified and isolated Pasteurellaceae polynucleotide comprising a nucleotide sequence selected from one of N1 to N68 or sequences which hybridize to them;

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 1/21, C07K 14/285, A61K 35/74, 39/02, C12N 15/63, 15/31, C07K 16/12, C12Q 1/18	A2	(11) International Publication Number: WO 00/61724 (43) International Publication Date: 19 October 2000 (19.10.00)
(21) International Application Number: PCT/US00/09218 (22) International Filing Date: 6 April 2000 (06.04.00) (30) Priority Data: 60/128,689 9 April 1999 (09.04.99) US 60/153,453 10 September 1999 (10.09.99) US (71) Applicant: PHARMACIA & UPJOHN, INC. [US/US]; 301 Henrietta Street, Kalamazoo, MI 49001 (US). (72) Inventors: LOWERY, David, E.; 1207 Woodland Drive, Portage, MI 49024 (US). FULLER, Troy, E.; 111 Dream- field Drive, Battle Creek, MI 49014 (US). KENNEDY, Michael, J.; 2364 Quincy Avenue, Portage, MI 49024 (US). (74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, O'Toole, Gerstein, Murray & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606-6402 (US).		(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS (57) Abstract Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.		

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☐ 1. Document ID: ZA 200108262 A, WO 200061724 A2, AU 200040776 A, EP 1171577 A2, BR 200009663 A, KR 2001112937 A, CN 1351653 A, JP 2002541790 W

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L4: Entry 1 of 1

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

INVENTOR: FULLER, T E; KENNEDY, M J ; LOWERY, D E

PRIORITY-DATA: 1999US-153453P (September 10, 1999), 1999US-128689P (April 9, 1999)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
ZA 200108262 A	March 26, 2003		337	C12N000/00
WO 200061724 A2	October 19, 2000	E	320	C12N001/21
AU 200040776 A	November 14, 2000		000	C12N001/21
EP 1171577 A2	January 16, 2002	E	000	C12N001/21
BR 200009663 A	April 9, 2002		000	C12N001/21
KR 2001112937 A	December 22, 2001		000	C12N001/21
CN 1351653 A	May 29, 2002		000	C12N001/21
JP 2002541790 W	December 10, 2002		341	C12N015/09

INT-CL (IPC): A61 K 35/74; A61 K 39/02; A61 K 39/102; A61 K 39/395; A61 P 31/04; C07 K 14/285; C07 K 16/12; C12 N 0/00; C12 N 1/15; C12 N 1/19; C12 N 1/21; C12 N 5/10; C12 N 15/01; C12 N 15/09; C12 N 15/31; C12 N 15/63; C12 P 21/02; C12 P 21/08; C12 Q 1/18; G01 N 33/15; G01 N 33/50; G01 N 33/53; G01 N 33/569; G01 N 33/577

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWC	Draw. Data
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L4: Entry 1 of 1

File: DWPI

Mar 26, 2003

DERWENT-ACC-NO: 2000-647422

DERWENT-WEEK: 200327

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TITLE: Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

Basic Abstract Text (1):

NOVELTY - A gram negative bacteria, such as attenuated Pasteurellaceae, comprising a mutation in a virulence gene, selected from one of 68 defined sequences (N1-N68) (given in the specification), is new.

Basic Abstract Text (4):

(2) a method for producing a gram-negative bacteria mutant, such as attenuated Pasteurellaceae, comprising introducing a mutation into any of N1 to N68, resulting in decreased activity of a gene product encoded by the mutated gene;

Basic Abstract Text (5):

(3) a purified and isolated Pasteurellaceae polynucleotide comprising a nucleotide sequence selected from one of N1 to N68 or sequences which hybridize to them;


Basic Abstract Text (16):

Nine groups of pigs were used to determine the safety and efficacy of seven A. pleuropneumoniae mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 1010 colony forming units (CFU) of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with 1-5 multiply 105 CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. ExbB, atpG, pnp, and yaeA mutants caused no mortality when administered at a dose of 1010 CFU intranasally. FkpA and tig mutant groups had one death each and the HI0379 group had four deaths. wildtype LD50 using this model was generally 1 multiply 107 CFU indicating that each of these mutants is at least 100 fold attenuated.

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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 1/21, C07K 14/285, A61K 35/74, 39/02, C12N 15/63, 15/31, C07K 16/12, C12Q 1/18	A2	(11) International Publication Number: WO 00/61724 (43) International Publication Date: 19 October 2000 (19.10.00)
(21) International Application Number: PCT/US00/09218 (22) International Filing Date: 6 April 2000 (06.04.00) (30) Priority Data: 60/128,689 9 April 1999 (09.04.99) US 60/153,453 10 September 1999 (10.09.99) US (71) Applicant: PHARMACIA & UPJOHN, INC. [US/US]; 301 Henrietta Street, Kalamazoo, MI 49001 (US). (72) Inventors: LOWERY, David, E.; 1207 Woodland Drive, Portage, MI 49024 (US). FULLER, Troy, E.; 111 Dreamfield Drive, Battle Creek, MI 49014 (US). KENNEDY, Michael, J.; 2364 Quincy Avenue, Portage, MI 49024 (US). (74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, O'Toole, Gerstein, Murray & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606-6402 (US).		(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS (57) Abstract Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.		

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Entry information

Entry name	ATPG_PASMU
Primary accession number	Q9L6B6
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	ATP synthase gamma chain
Synonym	EC 3.6.3.14
Gene name	ATPG or PM1493
From	<u>Pasteurella multocida</u> [TaxID: 747]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Pasteurellales</u> ; <u>Pasteurellaceae</u> ; <u>Pasteurella</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 Fuller T.E., Kennedy M.J., Lowery D.E.;
 "Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";
 Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
 STRAIN=Pm70;
 MEDLINE=21145866; PubMed=11248100; [NCBI, ExPASy, EBI, Israel, Japan]
 May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 "Complete genomic sequence of Pasteurella multocida Pm70.";
 Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Comments

- FUNCTION:** Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- **CATALYTIC ACTIVITY:** $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.
- **SUBUNIT:** F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
- **SIMILARITY:** Belongs to the ATPase gamma chain family.

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Cross-references

EMBL	AF237922; AAF68408.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE006186; AAK03577.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
CMR	Q9L6B6; PM1493.
InterPro	IPR000131 ; ATPase_gamma. Graphical view of domain structure.
Pfam	PF00231 ; ATP-synt; 1. Pfam graphical view of domain structure.
PRINTS	PR00126 ; ATPASEGAMMA.
TIGRFAMs	TIGR01146 ; ATPsyn_F1gamma; 1.
PROSITE	PS00153 ; ATPASE_GAMMA; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9L6B6 .
ProtoNet	Q9L6B6 .
ProtoMap	Q9L6B6 .
PRESAGE	Q9L6B6 .
DIP	Q9L6B6 .
ModBase	Q9L6B6 .
SMR	Q9L6B6 ; 1E1E862B4EEA9F70.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: **289** Molecular weight: **32095** CRC64: **1E1E862B4EEA9F70** [This is a checksum on the
AA Da sequence]

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70	80	90	100	110	120

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      130      140      150      160      170      180
      |      |      |      |      |      |
KSINFFQSLG IKILTQDSGI GDTPSVEQLI GSVNSMIDAY KKGEVDVVYL VYNKFINTMS
      190      200      210      220      230      240
      |      |      |      |      |      |
QKPVLEKLIP LPELDNDELG ERKQVWDYIY EPDAKVLLDN LLVRYLESQV YQAAVENLAS
      250      260      270      280
      |      |      |      |
EQAARMVAMK AATDNAGNLI NELQLVYNKA RQASITNELN EIVAGAAAI
```

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Hosted by YPRC Korea Mirror sites: Australia Bolivia Canada China Switzerland Taiwan USA				
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70	80	90	100	110	120

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130 140 150 160 170 180
| | | | | |
KSINFFQSLG IKILTQDSGI GDTPSVEQLI GSVNSMIDAY KKGEVDVVYL VYNKFINTMS
190 200 210 220 230 240
| | | | | |
QKPVLEKLIP LPELDNDELG ERKQVWDYIY EPDAKVLLDN LLVRYLESQV YQAAVENLAS
250 260 270 280
| | | |
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<input type="checkbox"/>	L2	atpg or atp-g	644
<input type="checkbox"/>	L3	L2.ti,ab,clm.	130
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		<i>DB=EPAB; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L5	WO-200061724-A2.did.	0
<input type="checkbox"/>	L6	BR-200009663-A.did.	0

END OF SEARCH HISTORY

0023] Any member of the Pasteurellaceae may be used according to the present invention. These include, without limitation members of the genus Actinobacillus, Bisgaard taxa, the genus Haemophilus, the genus Pasteurella, as well as unclassified members of the Pasteurellaceae, such as Pasteurellaceae gen. sp. CCUG28030, and Pasteurellaceae gen. sp. JF1390. Particularly important members of this family include P. haemolytica, P. multocida, P. pneumotropica, H. somnus, H. influenzae, H. parasuis, A. pleuropneumoniae, A. suis, and A. actinomycetemcomitans.

Brief Summary Text (22):

Described is a live vaccine against bacterial pathogens comprising a recombinant riboflavin-requiring mutant having a mutation that inactivates riboflavin biosynthesis therein. In particular, this includes bacterial pathogens in the family *Pasteurellaceae*, which include animal pathogens as *Actinobacillus pleuropneumoniae*, *Actinobacillus suis*, *Haemophilus parasuis*, *Pasteurella haemolytica* and *Pasteurella multocida*, as well as human pathogens *Haemophilus influenzae* and *Haemophilus ducreyi*.

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File: PGPB

Sep 18, 2003

DOCUMENT-IDENTIFIER: US 20030175835 A1

TITLE: Pathogen for bacterial poultry disease

Detail Description Paragraph:

[0043] The results of tests from sections A and B in the examples (Tables 1, 2 and 3) confirms the bacteria BIV-4895; ATCC No. PTA-3667 and BIV-AVICOR; ATCC No. PTA-3668 to belong to the family Pasteurellaceae (*Pasteurella trehalosi*, which are Trehalose positive and arabinose negative), while the bacteria BIV-07990; ATCC No. PTA-3669 belong to the family *Mannheimia* (*Mannheimia haemolytica*, which are Trehalose negative and arabinose negative).

Detail Description Paragraph:

[0087] The results of tests from Section A and B (Tables 1, 2 and 3) confirms the bacteria BIV-4895; ATCC No. PTA-3667 and BIV-AVICOR; ATCC No. PTA-3668 belong to the family Pasteurellaceae, (*Pasteurella trehalosi*, which are Trehalose positive and arabinose negative), while the bacteria BIV-07990; ATCC No. PTA-3669 belong to the family *Mannheimia* (*Mannheimia haemolytica*, which are Trehalose negative and arabinose negative). Identification of the Causative Agent

Summary of Invention Paragraph:

[0036] The mutant bacterium can be a Pasteurellaceae, e.g. the bacterium can be: *Pasteurella multocida*, *Pasteurella haemolytica*, *Pasteurella anatipestifer* or *Actinobacillus pleuropneumoniae*; advantageously *Pasteurella multocida*.

Summary of Invention Paragraph:

[0062] The invention concerns micro-organisms, such as bacteria, e.g., gram negative bacteria, such as bacteria of the Pasteurellaceae family, for instance, *Pasteurella multocida*, *Pasteurella haemolytica*, *Pasteurella anatipestifer* and *Actinobacillus pleuropneumoniae*. Advantageously the bacteria are *Pasteurella multocida*.

Summary of Invention Paragraph:

[0106] Heterologous nucleic acid sequences which are suitable for this use in such a vector will be apparent to the skilled person (Fedorova N D and Highlander S K, Infect Immun 1997, 65(7): 2593-8) and include for example those coming from Pasteurellaceae family members (notably *Pasteurella multocida*, *Pasteurella haemolytica*, *Pasteurella anatipestifer*, *Actinobacillus pleuropneumoniae*),

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L1: Entry 1 of 74

File: PGPB


Feb 19, 2004

DOCUMENT-IDENTIFIER: US 20040033994 A1

TITLE: Use of compounds comprising a nitrogen-oxygen heterocycle

CLAIMS:

13. Use according to claim 11 for the preparation of a pharmaceutical preparation for the treatment of infections, caused by bacteria, which are selected from the group, which consists of bacteria of the family Propionibacteriaceae, in particular the genus Propionibacterium, in particular species Propionibacterium acnes, bacteria of the family Actinomycetaceae, in particular the genus Actinomyces, bacteria of the genus Corynebacterium, in particular the species Corynebacterium diphtheriae and Corynebacterium pseudotuberculosis, bacteria of the family Mycobacteriaceae, the genus Mycobacterium, in particular the species Mycobacterium leprae, Mycobacterium tuberculosis, Mycobacterium bovis and Mycobacterium avium, bacteria of the family Chlamydiaceae, in particular the species Chlamydia trachomatis and Chlamydia psittaci, bacteria of the genus Listeria, in particular the species Listeria monocytogenes, bacteria of the species Erysipelthrix rhusiopathiae, bacteria of the genus Clostridium, bacteria of the genus Yersinia, of the species Yersinia pestis, Yersinia pseudotuberculosis, Yersinia enterocolitica enterocolitica and Yersinia ruckeri, bacteria of the family Mycoplasmataceae, of the the genera Mycoplasma and Ureaplasma, in particular the species Mycoplasma pneumoniae, bacteria of the genus Brucella, bacteria of the genus Bordetella, bacteria of the family Neisseriaceae, in particular of the genera Neisseria and Moraxella, in particular the species Neisseria meningitidis, Neisseria gonorrhoeae and Moraxella bovis, bacteria of the family Vibrionaceae, in particular of the genera Vibrio, Aeromonas, Plesiomonas and Photobacterium, in particular the species Vibrio cholerae, Vibrio anguillarum and Aeromonas salmonicida, bacteria of the genus Campylobacter, in particular the species Campylobacter jejuni, Campylobacter coli and Campylobacter fetus, bacteria of the genus Helicobacter, in particular the the species Helicobacter pylori, bacteria of the families Spirochaetaceae and Leptospiraceae, in particular the genera Treponema, Borrelia and Leptospira, in particular Borrelia burgdorferi, bacteria of the genus Actinobacillus, bacteria of the family Legionellaceae, the genus Legionella, bacteria of the family Rickettsiaceae and family Bartonellaceae, bacteria of the genera Nocardia and Rhodococcus, bacteria of the genus Dermatophilus, bacteria of the family Pseudomonadaceae, in particular the genera Pseudomonas and Xanthomonas, bacteria of the family Enterobacteriaceae, in particular the genera Escherichia, Klebsiella, Proteus, Providencia, Salmonella, Serratia and Shigella, bacteria of the family Pasteurellaceae, in particular the genus Haemophilus, bacteria of the family Micrococcaceae, in particular the genera Micrococcus and Staphylococcus, bacteria of the family Streptococcaceae, in particular the genera Streptococcus and Enterococcus and bacteria of the family Bacillaceae, in particular the genera Bacillus and Clostridium, and in the eradication of Helicobacter in ulcers of the gastrointestinal tract.

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Entry information

Entry name **ATPG_HAEIN**
 Primary accession number **P43716**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 32, November 1995
 Sequence was last modified in Release 32, November 1995
 Annotations were last modified in Release 41, February 2003

Name and origin of the protein

Protein name **ATP synthase gamma chain**
 Synonym **EC 3.6.3.14**
 Gene name **ATPG or HI0480**
 From **Haemophilus influenzae [TaxID: 727]**
 Taxonomy **Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800; [NCBI, ExPASy, EBI, Israel, Japan]
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
Science 269:496-512(1995).

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[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800; [NCBI, ExPASy, EBI, Israel, Japan]
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 "Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.";
Science 269:496-512(1995).

Comments

- **FUNCTION:** Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- **CATALYTIC ACTIVITY:** $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.
- **SUBUNIT:** F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
- **SIMILARITY:** Belongs to the ATPase gamma chain family.

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Cross-references

EMBL U32730; AAC22138.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR [E64071](#); E64071.
 TIGR [HI0480](#); -.
 InterPro [IPR000131](#); ATPase_gamma.
 Graphical view of domain structure.
 Pfam [PF00231](#); ATP-synt; 1.
 Pfam graphical view of domain structure.
 PRINTS [PR00126](#); ATPASEGAMMA.
 TIGRFAMs [TIGR01146](#); ATPsyn_F1gamma; 1.
 PROSITE [PS00153](#); ATPASE_GAMMA; 1.
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 HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]
 BLOCKS [P43716](#).
 ProtoNet [P43716](#).
 ProtoMap [P43716](#).
 PRESAGE [P43716](#).
 DIP [P43716](#).
 ModBase [P43716](#).
 SMR [P43716](#); 622CBA682F37FD00.
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: **289** Molecular weight: **32069** CRC64: **622CBA682F37FD00** [This is a checksum on the
 AA Da sequence]

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MAGAKEIKTK	IASVQSTQKI	TKAMEMVATS	KMRKTQDRMA	ASRPYSETIR	NVISHVSKAS
70	80	90	100	110	120

```

IGYKHPFLVE REVKKIGILV ISTDRGMCGG LNVNLFKTTL NQIKNWKEQN ISTDGLIGS
      130      140      150      160      170      180
      |      |      |      |      |      |
KGISFFRSFG FNIKGQLSGL GDTPALEELI GVANTMFDAY RNGEIDAVYI AYNKEVNTMS
      190      200      210      220      230      240
      |      |      |      |      |      |
QKPVVQQLVP LPESKDDHLN ERQQTWDYLY EPEPKVLLDS LLVRYLESQI YQAVVDNVAS
      250      260      270      280
      |      |      |      |
EQAARMVAMK AATDNAGNLI NDLRLVYNKA RQASITNELN EIVAGAAAI

```

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[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

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Entry information

Entry name	ATPG_PASMU
Primary accession number	Q9L6B6
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003
Name and origin of the protein	
Protein name	ATP synthase gamma chain
Synonym	EC 3.6.3.14
Gene name	ATPG or PM1493
From	<u>Pasteurella multocida</u> [TaxID: 747]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Pasteurellales</u> ; <u>Pasteurellaceae</u> ; <u>Pasteurella</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 Fuller T.E., Kennedy M.J., Lowery D.E.;
 "Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";
 Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=Pm70;
 MEDLINE=21145866; PubMed=11248100; [NCBI, ExPASy, EBI, Israel, Japan]
 May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Comments

- **FUNCTION:** Produces ATP from ADP in the presence of a proton gradient across the membrane.

The gamma chain is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex.

- **CATALYTIC ACTIVITY:** $\text{ATP} + \text{H}_2\text{O} + \text{H}^+(\text{In}) = \text{ADP} + \text{phosphate} + \text{H}^+(\text{Out})$.
- **SUBUNIT:** F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
- **SIMILARITY:** Belongs to the ATPase gamma chain family.

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Cross-references

EMBL AF237922; AAF68408.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 AE006186; AAK03577.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 CMR Q9L6B6; PM1493.
 InterPro IPR000131; ATPase_gamma.
 Graphical view of domain structure.
 Pfam PF00231; ATP-synt; 1.
 Pfam graphical view of domain structure.
 PRINTS PR00126; ATPASEGAMMA.
 TIGRFAMs TIGR01146; ATPsyn_F1gamma; 1.
 PROSITE PS00153; ATPASE_GAMMA; 1.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 BLOCKS Q9L6B6.
 ProtoNet Q9L6B6.
 ProtoMap Q9L6B6.
 PRESAGE Q9L6B6.
 DIP Q9L6B6.
 ModBase Q9L6B6.
 SMR Q9L6B6; 1E1E862B4EEA9F70.
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Keywords

ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; Complete proteome.

Features

None

Sequence information

Length: 289 Molecular weight: 32095 CRC64: 1E1E862B4EEA9F70 [This is a checksum on the
 AA Da sequence]

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70	80	90	100	110	120

IGYKHPFLVD REVKKVGMIV VSTDRLCGG LNVNLFKTVL NEMKEWKEKD VSVQLSLIGS

130 140 150 160 170 180
| | | | | |
KSINFFQSLG IKILTQDSGI GDTPSVEQLI GSVNSMIDAY KKGEVDVVYL VYNKFINTMS

190 200 210 220 230 240
| | | | | |
QKPVLEKLIP LPELDNDELG ERKQVWDYIY EPDAKVLLDN LLVRYLESQV YQAAVENLAS

250 260 270 280
| | | |
EQAARMVAMK AATDNAGNLI NELQLVYNKA RQASITNELN EIVAGAAAI


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Entry information

Entry name **Q83V88**
 Primary accession number **Q83V88**
 Secondary accession numbers None
 Entered in TrEMBL in Release 24, June 2003
 Sequence was last modified in Release 24, June 2003
 Annotations were last modified in Release 25, October 2003

Name and origin of the protein

Protein name **ATP synthase F1 epsilon subunit [Fragment]**
 Synonyms None
 Gene name **ATPG**
 From Haemophilus influenzae [TaxID: 727]
 Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=1158;
 MEDLINE=22683422; PubMed=12797973; [NCBI, ExPASy, EBI, Israel, Japan]
Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;
 "High rates of recombination in otitis media isolates of non-typeable *Haemophilus influenzae*."; Infect. Genet. Evol. 3:57-66(2003).

Comments

None

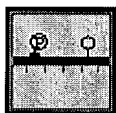
Cross-references

EMBL [AF535885](#); [AAP19744.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
[GO:0016020](#); Cellular component: membrane (*inferred from electronic annotation*).
 GO [GO:0015992](#); Biological process: proton transport (*inferred from electronic annotation*).

InterPro [IPR000131; ATPase_gamma.](#)
[Graphical view of domain structure.](#)
 Pfam [PF00231; ATP-synt; 1.](#)
[Pfam graphical view of domain structure.](#)
 PRINTS [PR00126; ATPASEGAMMA.](#)
 HOBACGEN [\[Family / Alignment / Tree\]](#)
 ProtoMap [Q83V88.](#)
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 SMR [Q83V88; 72005BDBF7066A3E.](#)
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Keywords

None

Features[Feature table viewer](#)

Key	From	To	Length	Description
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NON_TER	150	150		

Sequence information

Length: **150 AA** [This is the length of the partial sequence]
 Molecular weight: **16593 Da** [This is the MW of the partial sequence]
 CRC64: **72005BDBF7066A3E** [This is a checksum on the sequence]

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70	80	90	100	110	120
STDRGMCGGL	NVNLFKTTLN	QIKNWKEQNI	STDLGLIGSK	GISFFRSFGF	NIKGQLSGLG
130	140	150			
DTPALEELIG	VANTMFDAYR	NGEIDAIYIA			

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Entry information

Entry name **Q83U83**
 Primary accession number **Q83U83**
 Secondary accession numbers None
 Entered in TrEMBL in Release 24, June 2003
 Sequence was last modified in Release 24, June 2003
 Annotations were last modified in Release 25, October 2003

Name and origin of the protein

Protein name **ATP synthase F1 epsilon subunit [Fragment]**
 Synonyms None
 Gene name **ATPG**
 From Haemophilus influenzae [TaxID: 727]
 Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=1200, 1207, 1231, 1233, 1268, and 176;
MEDLINE=22683422; **PubMed**=12797973; [NCBI, ExPASy, EBI, Israel, Japan]
Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;
 "High rates of recombination in otitis media isolates of non-typeable *Haemophilus influenzae*."; *Infect. Genet. Evol.* 3:57-66(2003).

Comments

None

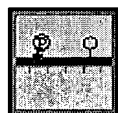
Cross-references

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	AF535890; AAP19749.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF535892; AAP19751.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

AF535894; AAP19753.1; [-.\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)
 GO [GO:0016020](#); Cellular component: membrane (*inferred from electronic annotation*).
[GO:0015992](#); Biological process: proton transport (*inferred from electronic annotation*).
 InterPro [IPR000131](#); ATPase_gamma.
[Graphical view of domain structure.](#)
 Pfam [PF00231](#); ATP-synt; 1.
[Pfam graphical view of domain structure.](#)
 PRINTS [PR00126](#); ATPASEGAMMA.
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 SMR [Q83U83](#); 72004DAA90066A3E.
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Keywords

None

Features[Feature table viewer](#)

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	150	150		

Sequence information

Length: **150 AA** [This is the length of the partial sequence] Molecular weight: **16621 Da** [This is the MW of the partial sequence] CRC64: **72004DAA90066A3E** [This is a checksum on the sequence]

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70	80	90	100	110	120
STDRGMCGGL	NVNLFKTTLN	QIKNWKEQNI	STDGLIGISK	GISFFRSFGF	NIKGQLSGLG
130	140	150			
DTPVLEELIG	VANTMFDAYR	NGEIDAIYIA			

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
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Entry information

Entry name	Q83U82
Primary accession number	Q83U82
Secondary accession numbers	None
Entered in TrEMBL in	Release 24, June 2003
Sequence was last modified in	Release 24, June 2003
Annotations were last modified in	Release 25, October 2003

Name and origin of the protein

Protein name	ATP synthase F1 epsilon subunit [Fragment]
Synonyms	None
Gene name	ATPG
From	<u>Haemophilus influenzae</u> [TaxID: 727]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Pasteurellales</u> ; <u>Pasteurellaceae</u> ; <u>Haemophilus</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=1124, 375, 477, and 723;

MEDLINE=22683422; PubMed=12797973; [NCBI, ExPASy, EBI, Israel, Japan]

Cody A.J., Field D., Feil E.J., Stringer S., Deadman M.E., Tsolaki A.G., Gratz B., Bouchet V., Goldstein R., Hood D.W., Moxon E.R.;

"High rates of recombination in otitis media isolates of non-typeable *Haemophilus influenzae*."; Infect. Genet. Evol. 3:57-66(2003).

Comments

None

Cross-references

EMBL

AF535898; AAP19757.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

AF535901; AAP19760.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

GO:0016020; Cellular component: membrane (*inferred from electronic annotation*).

GO:0015992; Biological process: proton transport (*inferred from electronic annotation*).

GO .

InterPro [IPR000131; ATPase_gamma.](#)
[Graphical view of domain structure.](#)

Pfam [PF00231; ATP-synt; 1.](#)
[Pfam graphical view of domain structure.](#)

PRINTS [PR00126; ATPASEGAMMA.](#)

HOBACGEN [\[Family / Alignment / Tree\]](#)

ProtoMap [Q83U82.](#)

PRESAGE [Q83U82.](#)

ModBase [Q83U82.](#)

SMR [Q83U82; 72005BC967066A3E.](#)

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UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

None

Features[Feature table viewer](#)

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	150	150		

Sequence information

Length: **150 AA** [This is the length of the partial sequence] Molecular weight: **16579 Da** [This is the MW of the partial sequence] CRC64: **72005BC967066A3E** [This is a checksum on the sequence]

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70	80	90	100	110	120
STDRGMCGL	NVNLFKTTLN	QIKNWKEQNI	STDGLIGISK	GISFFRSFGF	NIKGQLSGLG
130	140	150			
DTPALEELIG	VANTMFDAYR	NGEIDAVYIA			

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Entry information

Entry name	Q7VPP1
Primary accession number	Q7VPP1
Secondary accession numbers	None
Entered in TrEMBL in	Release 25, October 2003
Sequence was last modified in	Release 25, October 2003
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	ATP synthase gamma chain
Synonyms	None
Gene name	ATPG or HD0009
From	<u>Haemophilus ducreyi</u> [TaxID: <u>730</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Pasteurellales</u> ; <u>Pasteurellaceae</u> ; <u>Haemophilus</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R., Johnson L., Nguyen D., Wang J.,
Forst C., Hood L.;
 "The complete genome sequence of Haemophilus ducreyi."
 Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AE017151; AAP95033.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] GO:0016020 ; Cellular component: membrane (<i>inferred from electronic annotation</i>).
GO	GO:0015992 ; Biological process: proton transport (<i>inferred from electronic annotation</i>).
CMR	Q7VPP1 ; HD0009 .

InterPro [IPR000131; ATPase_gamma.](#)
[Graphical view of domain structure.](#)
Pfam [PF00231; ATP-synt; 1.](#)
[Pfam graphical view of domain structure.](#)
TIGRFAMs [TIGR01146; ATPsyn_F1gamma; 1.](#)
PROSITE [PS00153; ATPASE_GAMMA; 1.](#)
ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
HOBACGEN [\[Family / Alignment / Tree\]](#)
ProtoMap [Q7VPP1.](#)
PRESAGE [Q7VPP1.](#)
ModBase [Q7VPP1.](#)
SMR [Q7VPP1; 6CC7342402D4C977.](#)
SWISS-2DPAGE [Get region on 2D PAGE.](#)
UniRef [View cluster of proteins with at least 50% / 90% identity.](#)

Keywords**Complete proteome.****Features**

None

Sequence information

Length: **288** Molecular weight: **31953** CRC64: **6CC7342402D4C977** [This is a checksum on the AA Da sequence]

10	20	30	40	50	60
MAGAKEIRTK	IASVRNTQKI	TKAMEMVATS	KMRKTQERMA	AGRPYSETIR	KVISHIAKGS
70	80	90	100	110	120
IGYKHPFLIE	RDVKKVGYLV	ISTDRGLCGG	LNINLFKTTL	NEFKAWDKD	VSVELGLVGS
130	140	150	160	170	180
KGVSFYQSIG	LKVRAHITGL	GDSPEMERIV	GAVNEMINAY	RNGEVDMVCI	AYNRFENTMS
190	200	210	220	230	240
QKTVIAQLLP	LPKLENDELE	TKCSWDYLYE	PNPQVLLDSL	LIRYLETQVY	QAVVDNLASE
250	260	270	280		
QAARMVAMKA	ATDNAGALID	ELQLVYNKAR	QASITNELNE	IVAGAAAI	

Q7VPP1 in FASTA format


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 or at [NCBI \(USA\)](#)




[Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



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